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                 GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:         March 11, 2004, 03:37:21 ; Search time 353.257 Seconds
                                           (without alignments)
                                           15799.545 Million cell updates/sec

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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2432557 seqs, 1840798884 residues

Total number of hits satisfying chosen parameters:      4865114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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     Pred. No. is the number of results predicted by chance to have a
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     and is derived by analysis of the total score distribution.

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  No.   Score    Match  Length DB   ID                              Description
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   1     1515    99.9    1516  9   US-09-919-172-38                 Sequence 38, Appl
   2     1515    99.9    1516  9   US-09-974-298-92                 Sequence 92, Appl
   3     1515    99.9    1516  14   US-10-084-817-8                  Sequence 8, Appli
   4   1389.4    91.6    1399  9   US-09-864-864-321                Sequence 321, App
   5   1387.8    91.5    1399  9   US-09-954-456-2119               Sequence 2119, Ap
   6   1387.8    91.5    1399  14   US-10-240-965-2                  Sequence 2, Appli
   7   1387.8    91.5    1399  14   US-10-269-909-2                  Sequence 2, Appli
   8   1387.8    91.5    1399  15   US-10-133-937-2                  Sequence 2, Appli
   9   1387.8    91.5    1399  15   US-10-159-563-2                  Sequence 2, Appli
  10   1379.4    91.0    1431  9   US-09-925-301-46                 Sequence 46, Appl
  11   1367.4    90.2    1377  14   US-10-210-120-18                 Sequence 18, Appl
  12    886.8    58.5    1402  9   US-09-917-800A-1585              Sequence 1585, Ap
  13    886.8    58.5    1402  14   US-10-316-253-299                Sequence 299, App
  14      822    54.2    2500  10   US-09-814-353-20447              Sequence 20447, A
  15    597.4    39.4     600  12   US-10-085-783A-51438             Sequence 51438, A
  16    597.4    39.4     600  15   US-10-242-535A-51438             Sequence 51438, A
  17    589.4    38.9     614  9  US-09-864-864-241                 Sequence 241, App
  18    583.4    38.5     618  12   US-10-085-783A-13898             Sequence 13898, A
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  20      529    34.9     592  12   US-10-085-783A-48352             Sequence 48352, A
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c 22    519.4    34.3     537  9  US-09-777-564-134                 Sequence 134, App
c 23    519.4    34.3     537  14   US-10-015-219-134                Sequence 134, App
  24      505    33.3     557  12   US-10-085-783A-48313             Sequence 48313, A
  25      505    33.3     557  15   US-10-242-535A-48313             Sequence 48313, A
  26      500    33.0     530  12   US-10-085-783A-54108             Sequence 54108, A
  27      500    33.0     530  15   US-10-242-535A-54108             Sequence 54108, A
  28      496    32.7     590  12   US-10-085-783A-48227             Sequence 48227, A
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                              ALIGNMENTS

RESULT 1
US-09-919-172-38
; Sequence 38, Application US/09919172
; Patent No. US20020119463A1
; GENERAL INFORMATION:
;  APPLICANT: Faris, Mary
;  APPLICANT:  Turner, Christopher M.
;  TITLE OF INVENTION: PROSTATE CANCER MARKERS
;  FILE REFERENCE: PA-0036 US
;  CURRENT APPLICATION NUMBER: US/09/919,172
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: 60/222,469
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PERL Program
; SEQ ID NO 38
;   LENGTH: 1516
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20020119463A1 1303785CB1
;   NAME/KEY: unsure
;   LOCATION: 1512
;   OTHER INFORMATION: a, t, c, g, or other
US-09-919-172-38

  Query Match             99.9%;  Score 1515;  DB 9;  Length 1516;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1516;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 TCTGGTTGCTAGGTGTGGCTTCCTTTAAAATCCTATAAAATCAGAAGCCCAAGTCTCCAC 120
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Appendix A 2/2

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Qy        961 GAGTTGAAAGGTGACATTGAGAAATGCCTCACAGCTATCGTGAAGTGCGCCACAAGCAAA 1020
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Qy       1081 GCATTGATCAGGATTATGGTTTCCCGTTCTGAAATTGACATGAATGATATCAAAGCATTC 1140
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Db       1081 GCATTGATCAGGATTATGGTTTCCCGTTCTGAAATTGACATGAATGATATCAAAGCATTC 1140

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Qy       1501 AAAATAAAATGNCGTC 1516
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Db       1501 AAAATAAAATGNCGTC 1516


RESULT 2
US-09-974-298-92
; Sequence 92, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Huei-Mei
;  TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
;  FILE REFERENCE: PA-0037 P
;  CURRENT APPLICATION NUMBER: US/09/974,298
;  CURRENT FILING DATE:  2001-10-04
;  PRIOR APPLICATION NUMBER: 60/238,331
;  PRIOR FILING DATE: 2000-05-10
;  NUMBER OF SEQ ID NOS: 194
;  SOFTWARE: PERL Program
; SEQ ID NO 92
;   LENGTH: 1516
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20020156263A1 1303785CB1
;   NAME/KEY: unsure
;   LOCATION: 1512
;   OTHER INFORMATION: a, t, c, g, or other
US-09-974-298-92

  Query Match             99.9%;  Score 1515;  DB 9;  Length 1516;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1516;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        241 GAAAATGAAGAGCAGGAATATGTTCAAACTGTGAAGTCATCCAAAGGTGGTCCCGGATCA 300
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APPENDIX 3 1/2

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b      421 GCACAGCGTCAACAGATCAAAGCAGCATATCTCCAGGAAACAGGAAAGCCCCTGGATGAA 480

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b      841 GGGACAGACGTAAACGTGTTCAATACCATCCTTACCACCAGAAGCTATCCACAACTTCGC 900

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y     1141 TATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAAACCAAAGGAGAG 1200
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Qy       1201 TATGAGAAAATCCTGGTGGCTCTTTGTGGAGGAAACTAAACATTCCCTTGATGGTCTCAA 1260
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Db       1201 TATGAGAAAATCCTGGTGGCTCTTTGTGGAGGAAACTAAACATTCCCTTGATGGTCTCAA 1260

Qy       1261 GCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTT 1320

Qy       1321 CTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTT 1380
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Db       1321 CTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTT 1380

Qy       1381 TTATATTATAACTCTGTATAATAGAGATAAGTCCATTTTTTAAAAATGTTTTCCCCAAAC 1440
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Db       1381 TTATATTATAACTCTGTATAATAGAGATAAGTCCATTTTTTAAAAATGTTTTCCCCAAAC 1440

Qy       1441 CATAAAACCCTATACAAGTTGTTCTAGTAACAATACATGAGAAAGATGTCTATGTAGCTG 1500
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Db       1441 CATAAAACCCTATACAAGTTGTTCTAGTAACAATACATGAGAAAGATGTCTATGTAGCTG 1500

Qy       1501 AAAATAAAATGNCGTC 1516
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Db       1501 AAAATAAAATGNCGTC 1516

RESULT 2
US-09-974-298-92
; Sequence 92, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Huei-Mei
;  TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
;  FILE REFERENCE: PA-0037 P
;  CURRENT APPLICATION NUMBER: US/09/974,298
;  CURRENT FILING DATE:  2001-10-04
;  PRIOR APPLICATION NUMBER: 60/238,331
;  PRIOR FILING DATE: 2000-05-10
;  NUMBER OF SEQ ID NOS: 194
;  SOFTWARE: PERL Program
; SEQ ID NO 92
;   LENGTH: 1516
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20020156263A1 1303785CB1
;   NAME/KEY: unsure
;   LOCATION: 1512
;   OTHER INFORMATION: a, t, c, g, or other
US-09-974-298-92

  Query Match             99.9%;  Score 1515;  DB 9;  Length 1516;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1516;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 CTTTGTTTTTGGACATAGCTGAGCCATGTACTTCAAACAGAAGGCAGCCAATTACTAACT 60

Qy         61 TCTGGTTGCTAGGTGTGGCTTCCTTTAAAATCCTATAAAATCAGAAGCCCAAGTCTCCAC 120
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Db         61 TCTGGTTGCTAGGTGTGGCTTCCTTTAAAATCCTATAAAATCAGAAGCCCAAGTCTCCAC 120

Qy        121 TGCCAGTGTGAAATCTTCAGAGAAGAATTTCTCTTTAGTTCTTTGCAAGAAGGTAGAGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGCCAGTGTGAAATCTTCAGAGAAGAATTTCTCTTTAGTTCTTTGCAAGAAGGTAGAGAT 180

Qy        181 AAAGACACTTTTTCAAAAATGGCAATGGTATCAGAATTCCTCAAGCAGGCCTGGTTTATT 240
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Qy        241 GAAAATGAAGAGCAGGAATATGTTCAAACTGTGAAGTCATCCAAAGGTGGTCCCGGATCA 300
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APPENDIX B 2/2

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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          301 GCGGTGAGCCCCTATCCTACCTTCAATCCATCCTCGGATGTCGCTGCCTTGCATAAGGCC 360

y          361 ATAATGGTTAAAGGTGTGGATGAAGCAACCATCATTGACATTCTAACTAAGCGAAACAAT 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          361 ATAATGGTTAAAGGTGTGGATGAAGCAACCATCATTGACATTCTAACTAAGCGAAACAAT 420

y          421 GCACAGCGTCAACAGATCAAAGCAGCATATCTCCAGGAAACAGGAAAGCCCCTGGATGAA 480
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b          421 GCACAGCGTCAACAGATCAAAGCAGCATATCTCCAGGAAACAGGAAAGCCCCTGGATGAA 480

y          481 ACACTGAAGAAAGCCCTTACAGGTCACCTTGAGGAGGTTGTTTTAGCTCTGCTAAAAACT 540
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Qy         541 CCAGCGCAATTTGATGCTGATGAACTTCGTGCTGCCATGAAGGGCCTTGGAACTGATGAA 600
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Db         541 CCAGCGCAATTTGATGCTGATGAACTTCGTGCTGCCATGAAGGGCCTTGGAACTGATGAA 600

Qy         601 GATACTCTAATTGAGATTTTGGCATCAAGAACTAACAAAGAAATCAGAGACATTAACAGG 660
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Db         601 GATACTCTAATTGAGATTTTGGCATCAAGAACTAACAAAGAAATCAGAGACATTAACAGG 660

Qy         661 GTCTACAGAGAGGAACTGAAGAGAGATCTGGCCAAAGACATAACCTCAGACACATCTGGA 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         721 GATTTTCGGAACGCTTTGCTTTCTCTTGCTAAGGGTGACCGATCTGAGGACTTTGGTGTG 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 GATTTTCGGAACGCTTTGCTTTCTCTTGCTAAGGGTGACCGATCTGAGGACTTTGGTGTG 780

Qy         781 AATGAAGACTTGGCTGATTCAGATGCCAGGGCCTTGTATGAAGCAGGAGAAAGGAGAAAG 840
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Db         781 AATGAAGACTTGGCTGATTCAGATGCCAGGGCCTTGTATGAAGCAGGAGAAAGGAGAAAG 840

Qy         841 GGGACAGACGTAAACGTGTTCAATACCATCCTTACCACCAGAAGCTATCCACAACTTCGC 900
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Db         841 GGGACAGACGTAAACGTGTTCAATACCATCCTTACCACCAGAAGCTATCCACAACTTCGC 900

Qy         901 AGAGTGTTTCAGAAATACACCAAGTACAGTAAGCATGACATGAACAAAGTTCTGGACCTG 960
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Db         961 GAGTTGAAAGGTGACATTGAGAAATGCCTCACAGCTATCGTGAAGTGCGCCACAAGCAAA 1020

Qy        1021 CCAGCTTTCTTTGCAGAGAAGCTTCATCAAGCCATGAAAGGTGTTGGAACTCGCCATAAG 1080
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Qy        1081 GCATTGATCAGGATTATGGTTTCCCGTTCTGAAATTGACATGAATGATATCAAAGCATTC 1140
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Qy        1141 TATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAAACCAAAGGAGAG 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 TATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAAACCAAAGGAGAG 1200

Qy        1201 TATGAGAAAATCCTGGTGGCTCTTTGTGGAGGAAACTAAACATTCCCTTGATGGTCTCAA 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 TATGAGAAAATCCTGGTGGCTCTTTGTGGAGGAAACTAAACATTCCCTTGATGGTCTCAA 1260

Qy        1261 GCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTT 1320
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Db        1261 GCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTT 1320

Qy        1321 CTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTT 1380
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Qy        1381 TTATATTATAACTCTGTATAATAGAGATAAGTCCATTTTTTAAAAATGTTTTCCCCAAAC 1440
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Qy        1441 CATAAAACCCTATACAAGTTGTTCTAGTAACAATACATGAGAAAGATGTCTATGTAGCTG 1500
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Qy        1501 AAAATAAAATGNCGTC 1516
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Db        1501 AAAATAAAATGNCGTC 1516


RESULT 3
US-10-084-817-8
; Sequence 8, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
;  APPLICANT: Susan Stuart
;  APPLICANT:  Jed G. Nuchtern
;  APPLICANT:  Sharon E. Plon
;  APPLICANT:  Jason M. Shohet
;  TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
;  FILE REFERENCE: PA-0046 US
;  CURRENT APPLICATION NUMBER: US/10/084,817
;  CURRENT FILING DATE:  2002-02-25
;  PRIOR APPLICATION NUMBER: 60/270,784
;  PRIOR FILING DATE: 2001-02-23
;  NUMBER OF SEQ ID NOS: 365
;  SOFTWARE: PERL Program
; SEQ ID NO 8
;   LENGTH: 1516
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030119009A1 1303785CB1
;   NAME/KEY: unsure
;   LOCATION: 1512
;   OTHER INFORMATION: a, t, c, g, or other
US-10-084-817-8

  Query Match             99.9%;  Score 1515;  DB 14;  Length 1516;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1516;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy          61 TCTGGTTGCTAGGTGTGGCTTCCTTTAAAATCCTATAAAATCAGAAGCCCAAGTCTCCAC 120
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Qy         181 AAAGACACTTTTTCAAAAATGGCAATGGTATCAGAATTCCTCAAGCAGGCCTGGTTTATT 240
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Qy         241 GAAAATGAAGAGCAGGAATATGTTCAAACTGTGAAGTCATCCAAAGGTGGTCCCGGATCA 300
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Qy         361 ATAATGGTTAAAGGTGTGGATGAAGCAACCATCATTGACATTCTAACTAAGCGAAACAAT 420
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                     GenCore version 5.1.6
             Copyright (c) 1993 - 2004  Compugen Ltd.

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   Pred. No. is the number of results predicted by chance to have a
   score greater than or equal to the score of the result being printed,
   and is derived by analysis of the total score distribution.

                                    SUMMARIES
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sult              Query
 No.    Score     Match Length DB  ID                        Description
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   1     3693     100.0   3693  4  US-09-976-594-908         Sequence 908, App
   2    892.8      24.2    896  4  US-09-621-976-15155       Sequence 15155, A
   3    619.4      16.8    621  4  US-09-643-597-209         Sequence 209, App
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:  7    477.2      12.9    708  3  US-08-896-164-34          Sequence 34, Appl
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  14     66.8       1.8   2949  4  US-09-412-554A-3          Sequence 3, Appli
:  15    53.2       1.4   7218  1  US-08-232-463-14          Sequence 14, Appl
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:  17      47       1.3   1771  4  US-09-907-794A-158        Sequence 158, App
:  18      47       1.3   1771  4  US-09-866-028-36          Sequence 36, Appl
:  19      47       1.3   1771  4  US-09-905-125A-158        Sequence 158, App
:  20      47       1.3   1771  4  US-09-902-775A-158        Sequence 158, App
  21     45.8       1.2  11050  4  US-10-204-708-86          Sequence 86, Appl
:  22    45.6       1.2   5852  1  US-07-867-106-2           Sequence 2, Appli
)  23      45       1.2   6243  2  US-09-056-075-1           Sequence 1, Appli
  24     44.2       1.2   6801  4  US-10-204-708-62          Sequence 62, Appl
  25     44.2       1.2  11049  4  US-10-204-708-22          Sequence 22, Appl
:  26    43.8       1.2   1813  3  US-09-071-224-3           Sequence 3, Appli
  27     43.8       1.2   5152  4  US-10-204-708-47          Sequence 47, Appl
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   30    43.4     1.2    8607  4  US-10-204-708-72         Sequence 72, Appl
c  31    43.2     1.2   19124  2  US-08-487-826B-13        Sequence 13, Appl
   32      43     1.2    5666  4  US-10-204-708-30         Sequence 30, Appl
c  33    42.8     1.2     240  1  US-08-628-417-6          Sequence 6, Appli
c  34    42.8     1.2    1024  4  US-09-328-475C-50        Sequence 50, Appl
c  35    42.6     1.2    1440  4  US-09-252-991A-14965     Sequence 14965, A
   36    42.6     1.2    1545  4  US-09-252-991A-14667     Sequence 14667, A
   37    42.6     1.2    1767  4  US-09-252-991A-14785     Sequence 14785, A
c  38    42.4     1.1    1447  4  US-09-443-041A-27        Sequence 27, Appl
c  39    42.2     1.1   10640  4  US-09-417-485D-5         Sequence 5, Appli
   40    41.8     1.1     832  4  US-09-621-976-2813       Sequence 2813, Ap
   41    41.8     1.1    6326  4  US-10-204-708-57         Sequence 57, Appl
   42    41.8     1.1   11050  4  US-10-204-708-85         Sequence 85, Appl
   43    41.6     1.1   19233  4  US-10-204-708-46         Sequence 46, Appl
   44    41.6     1.1  640681  4  US-09-790-988-1          Sequence 1, Appli
   45    41.4     1.1     368  4  US-09-712-016-36         Sequence 36, Appl


                                ALIGNMENTS


RESULT 1
US-09-976-594-908
; Sequence 908, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;  APPLICANT: Furness, Michael
;  APPLICANT:  Buchbinder, Jenny
;  TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
;  FILE REFERENCE: PA-0041 US
;  CURRENT APPLICATION NUMBER: US/09/976,594
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: 60/240,409
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 1143
;  SOFTWARE: PERL Program
; SEQ ID NO 908
;   LENGTH: 3693
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673549 1505038CB1
US-09-976-594-908

  Query Match             100.0%;  Score 3693;  DB 4;  Length 3693;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3693;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGATCGGCGGACTCCCACCTCCGCTTACAGCTCGCTGCCGCCGTCCTGCCCCGCGCCCCC 60
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Db          1 CGATCGGCGGACTCCCACCTCCGCTTACAGCTCGCTGCCGCCGTCCTGCCCCGCGCCCCC 60

Qy         61 AGGAGACCTGGACCAGACCACGATGTGGAAACGCTGGCTCGCGCTCGCGCTCGCGCTGGT 120
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Qy        121 GGCGGTCGCCTGGGTCCGCGCCGAGGAAGAGCTAAGGAGCAAATCCAAGATCTGTGCCAA 180
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Qy        181 TGTGTTTTGTGGAGCCGGCCGGGAATGTGCAGTCACAGAGAAAGGGGAACCCACCTGTCT 240
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Db        181 TGTGTTTTGTGGAGCCGGCCGGGAATGTGCAGTCACAGAGAAAGGGGAACCCACCTGTCT 240

Qy        241 CTGCATTGAGCAATGCAAACCTCACAAGAGGCCTGTGTGTGGCAGTAATGGCAAGACCTA 300
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Db        241 CTGCATTGAGCAATGCAAACCTCACAAGAGGCCTGTGTGTGGCAGTAATGGCAAGACCTA 300

Qy        301 CCTCAACCACTGTGAACTGCATCGAGATGCCTGCCTCACTGGATCCAAAATCCAGGTTGA 360
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APPENDIX C 2/3

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   361 TTACGATGGACACTGCAAAGAGAAGAAATCCGTAAGTCCATCTGCCAGCCCAGTTGTTTG 420

   421 CTATCAGTCCAACCGTGATGAGCTCCGACGTCGCATCATCCAGTGGCTGGAAGCTGAGAT 480
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   421 CTATCAGTCCAACCGTGATGAGCTCCGACGTCGCATCATCCAGTGGCTGGAAGCTGAGAT 480

   481 CATCTCAGATGGCTGGTTCTCTAAAGGCAGCAACTACAGTGAAATCCTAGACAAGTATTT 540
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   541 TAAGAACTTTGATAATGGTGATTCTCGCCTGGACTCCAGTGAATTCCTGAAGTTTGTGGA 600

   601 ACAGAATGAAACTGCCATCAATATTACAACGTATCCAGACCAGGAGAACAACAAGTTGCT 660
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   901 GGGGGCCCAGACCCAGACAGAGGAGGAGATGACCAGATATGTCCAGGAGCTCCAAAAGCA 960
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Qy        1441 TTTCCATTGCCGTCAGCATGACAGACCTCCAGCATCCACGCATCTCTTGGTCCCAATAAC 1500
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APPENDIX C 3/3

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RESULT 2
US-09-621-976-15155
; Sequence 15155, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 15155
;   LENGTH: 896
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-15155

  Query Match             24.2%;  Score 892.8;  DB 4;  Length 896;
  Best Local Similarity   99.8%;  Pred. No. 2.1e-243;
  Matches  894;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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     Pred. No. is the number of results predicted by chance to have a
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     and is derived by analysis of the total score distribution.

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    2     3693    100.0    3693  14  US-10-084-817-20              Sequence 20, Appl
    3     1940     52.5    1987   9  US-09-880-107-3287            Sequence 3287, Ap
    4     1940     52.5    1987  10  US-09-960-706-941             Sequence 941, App
    5     1940     52.5    1987  10  US-09-873-319-617             Sequence 617, App
c   6   1729.8     46.8    2655  13  US-10-098-841-144             Sequence 144, App
    7   1678.4     45.4    1755   9  US-09-764-877-3903            Sequence 3903, Ap
    8   1678.4     45.4    1755  15  US-10-242-515-3903            Sequence 3903, Ap
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   13    619.4     16.8     621   9  US-09-850-716A-209            Sequence 209, App
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   17    619.4     16.8     621  15  US-10-313-986-209             Sequence 209, App
   18    543.2     14.7     589   9  US-09-738-973-546             Sequence 546, App
   19    543.2     14.7     589   9  US-09-854-133-546             Sequence 546, App
   20    543.2     14.7     589  14  US-10-144-649A-546            Sequence 546, App
c  21    477.2     12.9     708   9  US-09-835-992A-34             Sequence 34, Appl
   22    457.8     12.4     475  12  US-10-085-783A-56883          Sequence 56883, A
   23    457.8     12.4     475  15  US-10-242-535A-56883          Sequence 56883, A
   24    440.6     11.9     486  12  US-10-085-783A-56713          Sequence 56713, A
   25    440.6     11.9     486  15  US-10-242-535A-56713          Sequence 56713, A
   26    440.2     11.9     475  10  US-09-918-995-24257           Sequence 24257, A
   27      437     11.8     462  12  US-10-085-783A-37434          Sequence 37434, A
   28      437     11.8     462  15  US-10-242-535A-37434          Sequence 37434, A
   29    434.6     11.8     504  10  US-09-918-995-25431           Sequence 25431, A
   30    431.2     11.7     436  10  US-09-918-995-16944           Sequence 16944, A
   31    427.6     11.6     435  10  US-09-918-995-8663            Sequence 8663, Ap
   32    419.6     11.4     477  10  US-09-918-995-14933           Sequence 14933, A
   33    401.4     10.9     415  12  US-10-085-783A-24844          Sequence 24844, A
   34    401.4     10.9     415  15  US-10-242-535A-24844          Sequence 24844, A
   35    398.2     10.8     416  12  US-10-085-783A-16890          Sequence 16890, A
   36    398.2     10.8     416  15  US-10-242-535A-16890          Sequence 16890, A
   37    385.8     10.4     390  12  US-10-085-783A-42307          Sequence 42307, A
   38    385.8     10.4     390  15  US-10-242-535A-42307          Sequence 42307, A
   39    381.8     10.3     410  12  US-10-085-783A-51574          Sequence 51574, A
   40    381.8     10.3     410  15  US-10-242-535A-51574          Sequence 51574, A
   41    375.2     10.2     395  12  US-10-085-783A-12488          Sequence 12488, A
   42    375.2     10.2     395  15  US-10-242-535A-12488          Sequence 12488, A
   43      372     10.1     372  12  US-10-085-783A-21666          Sequence 21666, A
   44      372     10.1     372  15  US-10-242-535A-21666          Sequence 21666, A
   45      356      9.6     356  14  US-10-116-712-45              Sequence 45, Appl

                                  ALIGNMENTS


RESULT 1
US-09-919-039-359
; Sequence 359, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
;  APPLICANT: Kaser, Matthew R.
;  TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
;  FILE REFERENCE: PA-0035 US
;  CURRENT APPLICATION NUMBER: US/09/919,039
;  CURRENT FILING DATE:  2002-09-09
;  PRIOR APPLICATION NUMBER: 60/222,113
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 401
;  SOFTWARE: PERL Program
; SEQ ID NO 359
;   LENGTH: 3693
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030108871A1 1505038CB1
US-09-919-039-359

  Query Match             100.0%;  Score 3693;  DB 10;  Length 3693;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3693;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGATCGGCGGACTCCCACCTCCGCTTACAGCTCGCTGCCGCCGTCCTGCCCCGCGCCCCC 60
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Db          1 CGATCGGCGGACTCCCACCTCCGCTTACAGCTCGCTGCCGCCGTCCTGCCCCGCGCCCCC 60

Qy         61 AGGAGACCTGGACCAGACCACGATGTGGAAACGCTGGCTCGCGCTCGCGCTCGCGCTGGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGAGACCTGGACCAGACCACGATGTGGAAACGCTGGCTCGCGCTCGCGCTCGCGCTGGT 120

Qy        121 GGCGGTCGCCTGGGTCCGCGCCGAGGAAGAGCTAAGGAGCAAATCCAAGATCTGTGCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCGGTCGCCTGGGTCCGCGCCGAGGAAGAGCTAAGGAGCAAATCCAAGATCTGTGCCAA 180
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y      181 TGTGTTTTGTGGAGCCGGCCGGGAATGTGCAGTCACAGAGAAAGGGGAACCCACCTGTCT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      181 TGTGTTTTGTGGAGCCGGCCGGGAATGTGCAGTCACAGAGAAAGGGGAACCCACCTGTCT 240

y      241 CTGCATTGAGCAATGCAAACCTCACAAGAGGCCTGTGTGTGGCAGTAATGGCAAGACCTA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      241 CTGCATTGAGCAATGCAAACCTCACAAGAGGCCTGTGTGTGGCAGTAATGGCAAGACCTA 300

y      301 CCTCAACCACTGTGAACTGCATCGAGATGCCTGCCTCACTGGATCCAAAATCCAGGTTGA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      301 CCTCAACCACTGTGAACTGCATCGAGATGCCTGCCTCACTGGATCCAAAATCCAGGTTGA 360

y      361 TTACGATGGACACTGCAAAGAGAAGAAATCCGTAAGTCCATCTGCCAGCCCAGTTGTTTG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      361 TTACGATGGACACTGCAAAGAGAAGAAATCCGTAAGTCCATCTGCCAGCCCAGTTGTTTG 420

y      421 CTATCAGTCCAACCGTGATGAGCTCCGACGTCGCATCATCCAGTGGCTGGAAGCTGAGAT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      421 CTATCAGTCCAACCGTGATGAGCTCCGACGTCGCATCATCCAGTGGCTGGAAGCTGAGAT 480

y      481 CATCTCAGATGGCTGGTTCTCTAAAGGCAGCAACTACAGTGAAATCCTAGACAAGTATTT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      481 CATCTCAGATGGCTGGTTCTCTAAAGGCAGCAACTACAGTGAAATCCTAGACAAGTATTT 540

y      541 TAAGAACTTTGATAATGGTGATTCTCGCCTGGACTCCAGTGAATTCCTGAAGTTTGTGGA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      541 TAAGAACTTTGATAATGGTGATTCTCGCCTGGACTCCAGTGAATTCCTGAAGTTTGTGGA 600

y      601 ACAGAATGAAACTGCCATCAATATTACAACGTATCCAGACCAGGAGAACAACAAGTTGCT 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      601 ACAGAATGAAACTGCCATCAATATTACAACGTATCCAGACCAGGAGAACAACAAGTTGCT 660

y      661 TAGGGGACTCTGTGTTGATGCTCTCATTGAACTGTCTGATGAAAATGCTGATTGGAAACT 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      661 TAGGGGACTCTGTGTTGATGCTCTCATTGAACTGTCTGATGAAAATGCTGATTGGAAACT 720

y      721 CAGCTTCCAAGAGTTTCTCAAGTGCCTCAACCCATCTTTCAACCCTCCTGAGAAGAAGTG 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      721 CAGCTTCCAAGAGTTTCTCAAGTGCCTCAACCCATCTTTCAACCCTCCTGAGAAGAAGTG 780

y      781 TGCCCTGGAGGATGAAACGTATGCAGATGGAGCTGAGACCGAGGTGGACTGTAACCGCTG 840
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b      781 TGCCCTGGAGGATGAAACGTATGCAGATGGAGCTGAGACCGAGGTGGACTGTAACCGCTG 840

y      841 TGTCTGTGCCTGTGGAAATTGGGTCTGTACAGCCATGACCTGTGACGGAAAGAATCAGAA 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      841 TGTCTGTGCCTGTGGAAATTGGGTCTGTACAGCCATGACCTGTGACGGAAAGAATCAGAA 900

y      901 GGGGGCCCAGACCCAGACAGAGGAGGAGATGACCAGATATGTCCAGGAGCTCCAAAAGCA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      901 GGGGGCCCAGACCCAGACAGAGGAGGAGATGACCAGATATGTCCAGGAGCTCCAAAAGCA 960

y      961 TCAGGAAACAGCTGAAAAGACCAAGAGAGTGAGCACCAAAGAGATCTAATGAGGAGGCAC 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      961 TCAGGAAACAGCTGAAAAGACCAAGAGAGTGAGCACCAAAGAGATCTAATGAGGAGGCAC 1020

y     1021 AGACCAGTGTCTGGATCCCAGCATCTTCTCCACTTCAGCGCTGAGTTCAGTATACACAAG 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     1021 AGACCAGTGTCTGGATCCCAGCATCTTCTCCACTTCAGCGCTGAGTTCAGTATACACAAG 1080

y     1081 TGTCTGCTACAGTCGCCAAATCACCAGTATTTGCTTATATAGCAATGAGTTTTATTTTGT 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     1081 TGTCTGCTACAGTCGCCAAATCACCAGTATTTGCTTATATAGCAATGAGTTTTATTTTGT 1140

y     1141 TTATTTGTTTTGCAATAAAGGATATGAAGGTGGCTGGCTAGGAAGGGAAGGGCCACAGCC 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     1141 TTATTTGTTTTGCAATAAAGGATATGAAGGTGGCTGGCTAGGAAGGGAAGGGCCACAGCC 1200

y     1201 TTCATTTCTAGGAGTGCTTTAAGAGAAACTGTAAATGGTGCTCTGGGGCTGGAGGCTAGT 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     1201 TTCATTTCTAGGAGTGCTTTAAGAGAAACTGTAAATGGTGCTCTGGGGCTGGAGGCTAGT 1260
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Qy    1261 AAGGAAACTGCATCACGATTGAAAGAGGAACAGACCCAAATCTGAACCTCTTTTGAGTTT 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 AAGGAAACTGCATCACGATTGAAAGAGGAACAGACCCAAATCTGAACCTCTTTTGAGTTT 1320

Qy    1321 ACTGCATCTGTCAGCAGGCTGCAGGGAGTGCACACGATGCCAGAGAGAACTTAGCAGGGT 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 ACTGCATCTGTCAGCAGGCTGCAGGGAGTGCACACGATGCCAGAGAGAACTTAGCAGGGT 1380

Qy    1381 GTCCCCGGAGGAGAGGTTTGGGAAGCTCCACGGAGAGGAACGCTCTCTGCTTCCAGCCTC 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 GTCCCCGGAGGAGAGGTTTGGGAAGCTCCACGGAGAGGAACGCTCTCTGCTTCCAGCCTC 1440

Qy    1441 TTTCCATTGCCGTCAGCATGACAGACCTCCAGCATCCACGCATCTCTTGGTCCCAATAAC 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 TTTCCATTGCCGTCAGCATGACAGACCTCCAGCATCCACGCATCTCTTGGTCCCAATAAC 1500

Qy    1501 TGCCTCTAGATACATAGCCATACTGCTAGTTAACCCAGTGTCCCTCAGACTTGGATGGAG 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 TGCCTCTAGATACATAGCCATACTGCTAGTTAACCCAGTGTCCCTCAGACTTGGATGGAG 1560

Qy    1561 TTTCTGGGAGGGTACACCCAAATGATGCAGATACTTGTATACTTTGAGCCCCTTAGCGAC 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 TTTCTGGGAGGGTACACCCAAATGATGCAGATACTTGTATACTTTGAGCCCCTTAGCGAC 1620

Qy    1621 CTAACCAAATTTTAAAAATACTTTTTACCAAAGGTGCTATTTCTCTGTAAAACACTTTTT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 CTAACCAAATTTTAAAAATACTTTTTACCAAAGGTGCTATTTCTCTGTAAAACACTTTTT 1680

Qy    1681 TTTGGCAAGTTGACTTTATTCTTCAATTATTATCATTATATTATTGTTTTTTAATATTTT 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 TTTGGCAAGTTGACTTTATTCTTCAATTATTATCATTATATTATTGTTTTTTAATATTTT 1740

Qy    1741 ATTTTCTTGACTAGGTATTAAGCTTTTGTAATTATTTTTCAGTAGTCCCACCACTTCATA 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 ATTTTCTTGACTAGGTATTAAGCTTTTGTAATTATTTTTCAGTAGTCCCACCACTTCATA 1800

Qy    1801 GGTGGAAGGAGTTTGGGGTTCTTCCTGGTGCAGGGGCTGAAATAACCCAGATGCTCCCAC 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 GGTGGAAGGAGTTTGGGGTTCTTCCTGGTGCAGGGGCTGAAATAACCCAGATGCTCCCAC 1860

Qy    1861 CCTGCCACATACTAGATGCAGCCCATAGTTGGCCCCCCTAGCTTCCAGCAGTCCACTATC 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 CCTGCCACATACTAGATGCAGCCCATAGTTGGCCCCCCTAGCTTCCAGCAGTCCACTATC 1920

Qy    1921 TGCCAGAGGAGCAAGGGTGCCTTAGACCTAAGCCAGGGGAAGAAGCATCTTCATAAAAAA 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 TGCCAGAGGAGCAAGGGTGCCTTAGACCTAAGCCAGGGGAAGAAGCATCTTCATAAAAAA 1980

Qy    1981 CTTTCAAGATCCAAACATTAATTTGTTTTTATTTATTCTGAGAAGTTGAGGCAAATCAGT 2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 CTTTCAAGATCCAAACATTAATTTGTTTTTATTTATTCTGAGAAGTTGAGGCAAATCAGT 2040

Qy    2041 ATTCCCAAGGATGGCGACAAGGGCAGCCAAGCAGGGCTTAGGATATCCCAGCCTACCAAT 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 ATTCCCAAGGATGGCGACAAGGGCAGCCAAGCAGGGCTTAGGATATCCCAGCCTACCAAT 2100

Qy    2101 ATGCTCATTCGACTAACTAGGAGGGTGAGTTGGCCCTGTCTCTTCTTTTTTCTGGACCTC 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 ATGCTCATTCGACTAACTAGGAGGGTGAGTTGGCCCTGTCTCTTCTTTTTTCTGGACCTC 2160

Qy    2161 AGTTTCCTCAGTGAGCTGGTAAGAATGCACTAACCTTTTGATTTGATAAGTTATAAATTC 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161 AGTTTCCTCAGTGAGCTGGTAAGAATGCACTAACCTTTTGATTTGATAAGTTATAAATTC 2220

Qy    2221 TGTGGTTCTGATCATTGGTCCAGAGGGGAGATAGGTTCCTGTGATTTTTCCTTCTTCTCT 2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221 TGTGGTTCTGATCATTGGTCCAGAGGGGAGATAGGTTCCTGTGATTTTTCCTTCTTCTCT 2280

Qy    2281 ATAGAATAAATGAAATCTTGTTACTAGAACAAGAAATGTCAGATGGCCAAAAACAAGATG 2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 ATAGAATAAATGAAATCTTGTTACTAGAACAAGAAATGTCAGATGGCCAAAAACAAGATG 2340

Qy    2341 ACCAGATTTGATCTCAGCCTGATGACCCTACAGGTCGTGCTATGATATGGAGTCCTCATG 2400
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          2341 ACCAGATTTGATCTCAGCCTGATGACCCTACAGGTCGTGCTATGATATGGAGTCCTCATG 2400

y          2401 GGTAAAGCAGGAAGAGAGTGGGAAAGAGAACCACCCCACTCTGTCTTCATATTTGCATTT 2460
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          2401 GGTAAAGCAGGAAGAGAGTGGGAAAGAGAACCACCCCACTCTGTCTTCATATTTGCATTT 2460

y          2461 CATGTTTAACCTCCGGCTGGAAATAGAAAGCATTCCCTTAGAGATGAGGATAAAAGAAAG 2520
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          2461 CATGTTTAACCTCCGGCTGGAAATAGAAAGCATTCCCTTAGAGATGAGGATAAAAGAAAG 2520

y          2521 TTTCAGATTCAACAGGGGGAAGAAAATGGAGATTTAATCCTAAAACTGTGACTTGGGGAG 2580
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          2521 TTTCAGATTCAACAGGGGGAAGAAAATGGAGATTTAATCCTAAAACTGTGACTTGGGGAG 2580

y          2581 GTCAGTCATTTACAGTTAGTCCTGTGTCTTTCGACTTCTGTGATTATTAACCCCACTCAC 2640
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          2581 GTCAGTCATTTACAGTTAGTCCTGTGTCTTTCGACTTCTGTGATTATTAACCCCACTCAC 2640

y          2641 TACCCTGTTTCAGATGCATTTGGAATACCAAAGATTAAATCCTTGACATAAGATCTCATT 2700
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          2641 TACCCTGTTTCAGATGCATTTGGAATACCAAAGATTAAATCCTTGACATAAGATCTCATT 2700

y          2701 TGCAGAAAGCAGATTAAAGACCATCAGAAGGAAATTATTTAGGTTGTAATGCACAGGCAA 2760
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b          2701 TGCAGAAAGCAGATTAAAGACCATCAGAAGGAAATTATTTAGGTTGTAATGCACAGGCAA 2760

y          2761 CTGTGAGAAACTGTTGTGCCAAAAATAGAATTCCTTCTAGTTTTTCTTGTTCTCATTTGA 2820
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b          2761 CTGTGAGAAACTGTTGTGCCAAAAATAGAATTCCTTCTAGTTTTTCTTGTTCTCATTTGA 2820

y          2821 AAGGAGAAAATTCCACTTTGTTTAGCATTTCAAGCTTTTATGTATCCATCCCATCTAAAA 2880
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          2821 AAGGAGAAAATTCCACTTTGTTTAGCATTTCAAGCTTTTATGTATCCATCCCATCTAAAA 2880

y          2881 ACTCTTCAAACTCCACTTGTTCAGTCTGAAATGCAGCTCCCTGTCCAAGTGCCTTGGAGA 2940
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b          2881 ACTCTTCAAACTCCACTTGTTCAGTCTGAAATGCAGCTCCCTGTCCAAGTGCCTTGGAGA 2940

y          2941 ACTCACAGCAGCACGCCTTAATCAAAGGTTTTACCAGCCCTTGGACACTATGGGAGGAGG 3000
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          2941 ACTCACAGCAGCACGCCTTAATCAAAGGTTTTACCAGCCCTTGGACACTATGGGAGGAGG 3000

y          3001 GCAAGAGTACACCAATTTGTTAAAAGCAAGAAACCACAGTGTCTCTTCACTAGTCATTTA 3060
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          3001 GCAAGAGTACACCAATTTGTTAAAAGCAAGAAACCACAGTGTCTCTTCACTAGTCATTTA 3060

y          3061 GAACATGGTTATCATCCAAGACTACTCTACCCTGCAACATTGAACTCCCAAGAGCAAATC 3120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          3061 GAACATGGTTATCATCCAAGACTACTCTACCCTGCAACATTGAACTCCCAAGAGCAAATC 3120

y          3121 CACATTCCTCTTGAGTTCTGCAGCTTCTGTGTAAATAGGGCAGCTGTCGTCTATGCCGTA 3180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          3121 CACATTCCTCTTGAGTTCTGCAGCTTCTGTGTAAATAGGGCAGCTGTCGTCTATGCCGTA 3180

y          3181 GAATCACATGATCTGAGGACCATTCATGGAAGCTGCTAAATAGCCTAGTCTGGGGAGTCT 3240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          3181 GAATCACATGATCTGAGGACCATTCATGGAAGCTGCTAAATAGCCTAGTCTGGGGAGTCT 3240

y          3241 TCCATAAAGTTTTGCATGGAGCAAACAAACAGGATTAAACTAGGTTTGGTTCCTTCAGCC 3300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          3241 TCCATAAAGTTTTGCATGGAGCAAACAAACAGGATTAAACTAGGTTTGGTTCCTTCAGCC 3300

y          3301 CTCTAAAAGCATAGGGCTTAGCCTGCAGGCTTCCTTGGGCTTTCTCTGTGTGTGTAGTTT 3360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          3301 CTCTAAAAGCATAGGGCTTAGCCTGCAGGCTTCCTTGGGCTTTCTCTGTGTGTGTAGTTT 3360

y          3361 TGTAAACACTATAGCATCTGTTAAGATCCAGTGTCCATGGAAACCTTCCCACATGCCGTG 3420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          3361 TGTAAACACTATAGCATCTGTTAAGATCCAGTGTCCATGGAAACCTTCCCACATGCCGTG 3420

y          3421 ACTCTGGACTATATCAGTTTTTGGAAAGCAGGGTTCCTCTGCCTGCTAACAAGCCCACGT 3480
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Db         3421 ACTCTGGACTATATCAGTTTTTGGAAAGCAGGGTTCCTCTGCCTGCTAACAAGCCCACGT 3480

Qy         3481 GGACCAGTCTGAATGTCTTTCCTTTACACCTATGTTTTTAAGTAGTCAAACTTCAAGAAA 3540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3481 GGACCAGTCTGAATGTCTTTCCTTTACACCTATGTTTTTAAGTAGTCAAACTTCAAGAAA 3540

Qy         3541 CAATCTAAACAAGTTTCTGTTGCATATGTGTTTGTGAACTTGTATTTGTATTTAGTAGGC 3600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3541 CAATCTAAACAAGTTTCTGTTGCATATGTGTTTGTGAACTTGTATTTGTATTTAGTAGGC 3600

Qy         3601 TTCTATATTGCATTTAACTTGTTTTTGTAACTCCTGATTCTTCCTTTTCGGATACTATTG 3660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3601 TTCTATATTGCATTTAACTTGTTTTTGTAACTCCTGATTCTTCCTTTTCGGATACTATTG 3660

Qy         3661 ATGAATAAAGAAATTAAAGTGAAAAAAAAAAAA 3693
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Db         3661 ATGAATAAAGAAATTAAAGTGAAAAAAAAAAAA 3693


RESULT 2
US-10-084-817-20
; Sequence 20, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
;  APPLICANT: Susan Stuart
;  APPLICANT:  Jed G. Nuchtern
;  APPLICANT:  Sharon E. Plon
;  APPLICANT:  Jason M. Shohet
;  TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
;  FILE REFERENCE: PA-0046 US
;  CURRENT APPLICATION NUMBER: US/10/084,817
;  CURRENT FILING DATE:  2002-02-25
;  PRIOR APPLICATION NUMBER: 60/270,784
;  PRIOR FILING DATE: 2001-02-23
;  NUMBER OF SEQ ID NOS: 365
;  SOFTWARE: PERL Program
; SEQ ID NO 20
;   LENGTH: 3693
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030119009A1 1505038CB1
US-10-084-817-20

  Query Match             100.0%;  Score 3693;  DB 14;  Length 3693;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3693;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy            1 CGATCGGCGGACTCCCACCTCCGCTTACAGCTCGCTGCCGCCGTCCTGCCCCGCGCCCCC 60
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Db            1 CGATCGGCGGACTCCCACCTCCGCTTACAGCTCGCTGCCGCCGTCCTGCCCCGCGCCCCC 60

Qy           61 AGGAGACCTGGACCAGACCACGATGTGGAAACGCTGGCTCGCGCTCGCGCTCGCGCTGGT 120
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Qy          121 GGCGGTCGCCTGGGTCCGCGCCGAGGAAGAGCTAAGGAGCAAATCCAAGATCTGTGCCAA 180
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Qy          181 TGTGTTTTGTGGAGCCGGCCGGGAATGTGCAGTCACAGAGAAAGGGGAACCCACCTGTCT 240
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Qy          241 CTGCATTGAGCAATGCAAACCTCACAAGAGGCCTGTGTGTGGCAGTAATGGCAAGACCTA 300
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Qy          301 CCTCAACCACTGTGAACTGCATCGAGATGCCTGCCTCACTGGATCCAAAATCCAGGTTGA 360
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                      GenCore version 5.1.6
             Copyright (c) 1993 - 2004  Compugen Ltd.

M nucleic - nucleic search, using sw model

un on:         March 11, 2004, 03:37:21 ; Search time 298.498 Seconds
                                          (without alignments)
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coring table:  IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

earched:       2432557 seqs, 1840798884 residues

otal number of hits satisfying chosen parameters:      4865114

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries

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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                  SUMMARIES
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Result                Query
  No.     Score       Match Length DB  ID                            Description
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    1      1281      100.0    1281  14  US-10-084-817-1              Sequence 1, Appli
    2    1255.8       98.0    1308  14  US-10-102-806-120            Sequence 120, App
    3     398.6       31.1     475  10  US-09-918-995-23651          Sequence 23651, A
    4     394.2       30.8     407  10  US-09-918-995-16444          Sequence 16444, A
    5       105        8.2     469  14  US-10-198-846-11619          Sequence 11619, A
c   6      76.4        6.0     906  14  US-10-198-846-3098           Sequence 3098, Ap
    7        60        4.7      60  10  US-09-908-975-8225           Sequence 8225, Ap
    8        51        4.0    2100  12  US-10-282-122A-25713         Sequence 25713, A
c   9      50.6        4.0    2057  15  US-10-027-632-110305         Sequence 110305,
c  10      50.6        4.0    2057  15  US-10-027-632-110306         Sequence 110306,
c  11      48.2        3.8     500  10  US-09-991-936-317            Sequence 317, App
   12      47.4        3.7   22693  12  US-10-271-416-6              Sequence 6, Appli
   13      43.6        3.4     830  12  US-10-425-114-831            Sequence 831, App
   14      42.2        3.3     671  14  US-10-184-644-346            Sequence 346, App
   15      42.2        3.3     671  14  US-10-184-634-346            Sequence 346, App
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     16     41.8      3.3    1184  14  US-10-123-155-412          Sequence 412, App
     17     41.8      3.3    1184  14  US-10-146-731-412          Sequence 412, App
     18     41.8      3.3    1184  14  US-10-140-472-412          Sequence 412, App
     19     41.8      3.3    1184  14  US-10-141-761-412          Sequence 412, App
     20     41.8      3.3    1184  14  US-10-142-885-412          Sequence 412, App
     21     41.8      3.3    1184  14  US-10-158-790-412          Sequence 412, App
     22     41.8      3.3    1184  15  US-10-137-871-412          Sequence 412, App
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     33     40.2      3.1     653  14  US-10-184-644-402          Sequence 402, App
     34     40.2      3.1     653  14  US-10-184-634-402          Sequence 402, App
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                                ALIGNMENTS


RESULT 1
US-10-084-817-1
; Sequence 1, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
;  APPLICANT: Susan Stuart
;  APPLICANT:  Jed G. Nuchtern
;  APPLICANT:  Sharon E. Plon
;  APPLICANT:  Jason M. Shohet
;  TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
;  FILE REFERENCE: PA-0046 US
;  CURRENT APPLICATION NUMBER: US/10/084,817
;  CURRENT FILING DATE:  2002-02-25
;  PRIOR APPLICATION NUMBER: 60/270,784
;  PRIOR FILING DATE: 2001-02-23
;  NUMBER OF SEQ ID NOS: 365
;  SOFTWARE: PERL Program
; SEQ ID NO 1
;   LENGTH: 1281
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030119009A1 1497123CB1
US-10-084-817-1

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  Matches 1281;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 GTTCTGGGCGGGGCTGGACTGTTCTAAGTGAGTTCGGGTGGGGGAGCTTCACGAGGGGAG 60

Qy         61 GCTGCTCTGTGAAGGAACCGCCTTTCTCTCCGCGTGTCTCACCCTTTTCTCCCCATATCT 120
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Qy      121 GTTTGGACATGAGCTGAGGGCACGGTCGCGGGCGGTCAGCCCTGTTCGCAGCTACGGCGA 180
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Qy      781 ACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGC 840
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Qy      841 AGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTG 900
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Db      841 AGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTG 900

Qy      901 AGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGAT 960
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Qy      961 CCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATT 1020
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Qy     1081 TCAGGAGGAGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCT 1140
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; Sequence 120, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA103P1C1
;  CURRENT APPLICATION NUMBER: US/10/102,806
;  CURRENT FILING DATE:  2002-03-22
;  PRIOR APPLICATION NUMBER: 09/925,298
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05881
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 846
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
;   LENGTH: 1308
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-102-806-120

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Qy        9 CGGGGCTGGACTGTTCTAAGTGAGTTCGGGTGGGGAGCTTCACGAGGGGAGGCTGCTCT 68
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Qy      369 GACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCCGG 428
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Db      428 CTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGACTC 487

Qy      489 CTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGAGAGGAG 548
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Db      488 CTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGAGAGGAG 547

Qy      549 AAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGCCC 608
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y         609 ATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAGGCCTAT 668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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y         669 GGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCAGCGGGGC 728
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y         729 TGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGG 788
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y         789 GACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAG 848
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b         788 GACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAG 847

y         849 AACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGG 908
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b         848 AACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGG 907

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y         969 AGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGG 1028
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y        1029 CAGGAAACCTCTGGAGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGG 1088
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y        1149 CCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCC 1208
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y        1209 CTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCA 1268
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b        1208 CTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCA 1267

y        1269 CAAAAAAAAAAAA 1281
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b        1268 CAAAAAAAAAAAA 1280

ESULT 3
S-09-918-995-23651
 Sequence 23651, Application US/09918995
 Publication No. US20030073623A1
 GENERAL INFORMATION:
  APPLICANT: Hyseq, Inc.
  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
  FILE REFERENCE: 20411-756
  CURRENT APPLICATION NUMBER: US/09/918,995
  CURRENT FILING DATE:  2001-07-30
  PRIOR APPLICATION NUMBER: US/09/235,076
  PRIOR FILING DATE: 1999-01-20
  NUMBER OF SEQ ID NOS: 38054
  SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 23651
   LENGTH: 475
   TYPE: DNA
   ORGANISM: Homo sapiens
   FEATURE:
   NAME/KEY: misc_feature
```

```
;    LOCATION: (1)...(475)
;    OTHER INFORMATION: n = A,T,C or G
US-09-918-995-23651

  Query Match             31.1%;  Score 398.6;  DB 10;  Length 475;
  Best Local Similarity   97.8%;  Pred. No. 7.9e-109;
  Matches  404;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy        869 CTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGG 928
              |||  |   ||   ||| ||||||||||||||||||||||||||||||||||||||||||
Db         34 CTCGCGGAATTCCGCACGAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGG 93

Qy        929 GCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGACAGGGG 988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 GCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGACAGGGG 153

Qy        989 GGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGGAGACCT 1048
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 GGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGGAGACCT 213

Qy       1049 CATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCAAAGGAG 1108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 CATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCAAAGGAG 273

Qy       1109 GGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCCCCTCAG 1168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 GGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCCCCTCAG 333

Qy       1169 CCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCC 1228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCC 393

Qy       1229 AGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACAAAAAAAAAAAA 1281
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 AGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACAAAAAAAAAAAA 446


RESULT 4
US-09-918-995-16444
; Sequence 16444, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16444
;   LENGTH: 407
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-918-995-16444

  Query Match             30.8%;  Score 394.2;  DB 10;  Length 407;
  Best Local Similarity   98.0%;  Pred. No. 1.6e-107;
  Matches  399;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy        129 ATGAGCTGAGGGCACGGTCGCGGGCGGTCAGCCCTGTTCGCAGCTACGGCGAGGAGGGGC 188
              | ||||||||||||||||||||||||| |||||||||||||  |||||||||||||||||
Db          1 ACGAGCTGAGGGCACGGTCGCGGGCGGCCAGCCCTGTTCGCTTCTACGGCGAGGAGGGGC 60

Qy        189 GCGATTGTTCCTTGTTGCCGCTCCGCTTAGTGGCCGCGTCCATTCCGCGCGGTGTCCCGA 248
              ||||||| |||||| ||||||||||||||||||||||||||||||||||||| |||||||
Db         61 GCGATTGCTCCTTGCTGCCGCTCCGCTTAGTGGCCGCGTCCATTCCGCGCGGCGTCCCGA 120

Qy        249 TTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGGCC 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGGCC 180
```

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Qy        309 CCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGAAG 368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGAAG 240

Qy        369 GACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCCGG 428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCCGG 300

Qy        429 CTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGACTC 488
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        301 CTCTCTGGTCCACTCAAGGAACAGTATGCTCATGAGCATGGCTTGAACTTCCAGAGACTC 360

Qy        489 CTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCG 535
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCG 407

RESULT 5
US-10-198-846-11619
; Sequence 11619, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
;  APPLICANT: Lillie, James
;  APPLICANT:  Xu, Yongyao
;  APPLICANT:  Wang, Youzhen
;  APPLICANT:  Steinmann, Kathleen
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
;  TITLE OF INVENTION:  FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;  TITLE OF INVENTION:  THERAPY OF BREAST CANCER
;  FILE REFERENCE: MRI-049
;  CURRENT APPLICATION NUMBER: US/10/198,846
;  CURRENT FILING DATE:  2002-07-18
;  PRIOR APPLICATION NUMBER: 60/306,220
;  PRIOR FILING DATE: 2001-07-18
;  NUMBER OF SEQ ID NOS: 14084
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11619
;   LENGTH: 469
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1, 2, 3, 4
;   OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11619

  Query Match             8.2%;  Score 105;  DB 14;  Length 469;
  Best Local Similarity   95.6%;  Pred. No. 4.6e-21;
  Matches  108;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        357 AAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGT 416
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 AAATCCGGAAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGT 64

Qy        417 GCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGG 469
              ||||||||||||||||||||||||||||||||||||||||||||||    |||
Db         65 GCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGTAGGTGG 117

RESULT 6
US-10-198-846-3098/c
; Sequence 3098, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
;  APPLICANT: Lillie, James
;  APPLICANT:  Xu, Yongyao
;  APPLICANT:  Wang, Youzhen
;  APPLICANT:  Steinmann, Kathleen
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
;  TITLE OF INVENTION:  FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;  TITLE OF INVENTION:  THERAPY OF BREAST CANCER
;  FILE REFERENCE: MRI-049
;  CURRENT APPLICATION NUMBER: US/10/198,846
;  CURRENT FILING DATE:  2002-07-18
;  PRIOR APPLICATION NUMBER: 60/306,220
;  PRIOR FILING DATE: 2001-07-18
;  NUMBER OF SEQ ID NOS: 14084
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3098
;   LENGTH: 906
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1, 24, 346, 350, 495, 630, 632, 638, 640, 657, 663, 684,
;   LOCATION: 691, 718, 721, 736, 755, 762, 766, 780, 817, 825, 826, 845,
;   LOCATION: 849, 864, 874, 879, 881, 894, 897, 904, 905
;   OTHER INFORMATION: n = A,T,C or G
US-10-198-846-3098

  Query Match             6.0%;  Score 76.4;  DB 14;  Length 906;
  Best Local Similarity   76.8%;  Pred. No. 1.9e-12;
  Matches  119;  Conservative    0;  Mismatches   32;  Indels    4;  Gaps    2;

Qy        319 GCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGAA--GGACTTCGT 376
              |||  ||| || |  |       |     ||||||||||||||||||||  |   |||||
Db        566 GCGGGCCGAGGGTACTTGCTTGTTCAGCGGGCAAGAGGAAATCCGGGAAAGGACTTTCGT 507

Qy        377 GACCGA--GGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCCGGCTCTCT 434
              ||||||  |       ||||||||||||||||||||||||||||||||||||||||||||
Db        506 GACCGAAGGCGNTGCAAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCCGGCTCTCT 447

Qy        435 GGTCCACTCAAGGAACAGTATGCTCAGGAGCATGG 469
              ||||||||||||||||||||||||||||    |||
Db        446 GGTCCACTCAAGGAACAGTATGCTCAGGTAGGTGG 412

RESULT 7
US-09-908-975-8225
; Sequence 8225, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
;  APPLICANT: SHOSHAN, Avi
;  APPLICANT:  WASSERMAN, Alon
;  APPLICANT:  MINTZ, Eli
;  APPLICANT:  MINTZ, Liat
;  APPLICANT:  FAIGLER, Simchon
;  TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
;  TITLE OF INVENTION:  THAT POPULATE A TRANSCRIPTOME
;  FILE REFERENCE: 36688-0005
;  CURRENT APPLICATION NUMBER: US/09/908,975
;  CURRENT FILING DATE:  2001-07-20
;  PRIOR APPLICATION NUMBER: US 60/287,724
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: US 60/221,607
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 32337
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8225
;   LENGTH: 60
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-908-975-8225

  Query Match             4.7%;  Score 60;  DB 10;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-08;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1194 GGATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGTGGATACTAAT 1253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGTGGATACTAAT 60

RESULT 8
US-10-282-122A-25713
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```
; Sequence 25713, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
;  APPLICANT:  Yamamoto, Robert
;  APPLICANT:  Forsyth, R.
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25713
;   LENGTH: 2100
;   TYPE: DNA
;   ORGANISM: Mycobacterium avium
US-10-282-122A-25713

  Query Match              4.0%;  Score 51;  DB 12;  Length 2100;
  Best Local Similarity   52.5%;  Pred. No. 9.4e-05;
  Matches  134;  Conservative    0;  Mismatches  120;  Indels    1;  Gaps    1;

Qy        121 GTTTGGACATGAGCTGAGGGCACGGTCGCGGGCGGTCAGCCCTGTTCGCAGCTACGGCGA 180
              ||| |   | |||| | | | |  | | | || || | ||   |     |    | ||||
Db       1620 GTTCGCCAAGGAGCGGCGCGAAGAGGCCCTGGAGGCCGGCAAGGACGCGATGGCCCGCGA 1679

Qy        181 GGAGGGGCGCGATTGTTCCTTGTTGCCGCTCCGCTTAGTGGCCGCGTCCATTCCGCGCGG 240
              || | | ||||   |      ||||| || |    |    ||||  |||| |  ||||||
Db       1680 GGTGCGCCGCGGCGGACTTCCGTTGCAGCGCTTGGTCAATGCCGAATCCA-TGAGCGCGG 1738

Qy        241 TGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCC 300
              || ||||      |   || |  || ||||| ||      || |||||   |||  || |
Db       1739 TGGCCCGCGAACTGCACTACGCCGACGTGTCGGCCCTCTACACCGCGATCGGTGAGGGGC 1798

Qy        301 CCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAAT 360
                 || |  | | |   |  |  | ||||||| |      | || ||||||      |
Db       1799 ATGTGTCGGCCCGGCACGTGGTGCAGCGGCTGCTGGCCGAGCTCGGCGGCATCGACCAGG 1858

Qy        361 CCGGGAAGGACTTCG 375
              ||| | ||||| |||
Db       1859 CCGAGGAGGACCTCG 1873

RESULT 9
US-10-027-632-110305/c
; Sequence 110305, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 110305
;   LENGTH: 2057
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(2057)
;   OTHER INFORMATION: n = A,T,C or G
US-10-027-632-110305

  Query Match              4.0%;  Score 50.6;  DB 15;  Length 2057;
  Best Local Similarity   40.0%;  Pred. No. 0.00012;
  Matches  206;  Conservative    0;  Mismatches  309;  Indels    0;  Gaps    0;

Qy        345 AGCGGCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGA 404
              || |||  |||||    | |||||||    | |   |||| |  || ||        ||
Db        979 AGGGGCTGGAGGAGGGGCTGGAAGGAGGAAGGGCTGGAGGAGGGGCTGAAGGAGGAGGGG 920

Qy        405 GCTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAG 464
                 ||||     ||| | | |  ||     |     ||   |||  || |
Db        919 CTCGATGCTGAGGCTCTGCGCGAGCCGGAGGAGGGGCTGTTGGAGGAGGAGNNNNNNNNN 860

Qy        465 CATGGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAG 524
                                                         ||||||          |
Db        859 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGGAGGAGGAGGAGGACCTG 800

Qy        525 GACATGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAG 584
              |    |    ||  ||||||||||||| ||| || |||    |    | |      | ||
Db        799 GGAGAGGAGGGCCTGGGAGAGGAGAAAGGCCTGGATGAGGAGGAGGGCCTGGAGGAGGAG 740

Qy        585 ATTGTGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGAC 644
                 | |  |||        | |  | |  |  || |        | |  |||||   ||
Db        739 GAGGGGCTGGGAGAGGAGGACCTGAACGAGAAGGAGGAGCCAGAAGGAGGAGTGGAGGAG 680

Qy        645 ATCCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTG 704
              |   ||  |     |||||     ||||  | |  | ||            |  | | ||
Db        679 AAGGAGGAGCAGGAGGAGGAGCTGGGGGAAGAGGAGGAGCTAAGAAAGAAGGAGGAGATG 620

Qy        705 GAGCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCA 764
              ||| ||    | | | | |  | |   || ||   | |   | || |   |  || |||
Db        619 GAGGAGGAGGGGCTGGATGGTGAGGGGCTGGGAAAGGAGGAGGGGCTGGGAGCGGAGGTG 560

Qy        765 GAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAA 824
              | | | ||    | ||     |  |    |||   |||  | || ||  | |  |   |
Db        559 GGAGGAGGGGCTGGCAGAGGAGAAGGGGCTGAGGAGGTACTGGAAAAGAAAGAGGAGCAG 500
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Qy        825 CAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGA 859
               |||    ||| ||   |  |||| | |||   ||
Db        499 GAGCTGGAGGAAGACGTGGAGGAGGAGCTGGAGGA 465

RESULT 10
US-10-027-632-110306/c
; Sequence 110306, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 110306
;   LENGTH: 2057
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(2057)
;   OTHER INFORMATION: n = A,T,C or G
US-10-027-632-110306

  Query Match              4.0%;  Score 50.6;  DB 15;  Length 2057;
  Best Local Similarity   40.0%;  Pred. No. 0.00012;
  Matches  206;  Conservative    0;  Mismatches  309;  Indels    0;  Gaps    0;

Qy        345 AGCGGCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGA 404
              || |||  |||||    | |||||||    | |   |||| |  || ||        ||
Db        979 AGGGGCTGGAGGAGGGGCTGGAAGGAGGAAGGGCTGGAGGAGGGGCTGAAGGAGGAGGGG 920

Qy        405 GCTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAG 464
                 ||||     ||| | | |  ||     |     ||   |||  || |
Db        919 CTCGATGCTGAGGCTCTGCGCGAGCCGGAGGAGGGGCTGTTGGAGGAGGAGNNNNNNNNN 860

Qy        465 CATGGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAG 524
                                                         ||||||          |
Db        859 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGGAGGAGGAGGAGGACCTG 800

Qy        525 GACATGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAG 584
              |    |    ||  ||||||||||||| ||| || |||    |    | |      | ||
Db        799 GGAGAGGAGGGCCTGGGAGAGGAGAAAGGCCTGGATGAGGAGGAGGGCCTGGAGGAGGAG 740

Qy        585 ATTGTGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGAC 644
                 | |  |||        | |  | |  |  || |        | |  |||||   ||
Db        739 GAGGGGCTGGGAGAGGAGGACCTGAACGAGAAGGAGGAGCCAGAAGGAGGAGTGGAGGAG 680

Qy        645 ATCCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTG 704
              |   ||  |     |||||     ||||  | |  | ||            |  | | ||
Db        679 AAGGAGGAGCAGGAGGAGGAGCTGGGGGAAGAGGAGGAGCTAAGAAAGAAGGAGGAGATG 620

Qy        705 GAGCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCA 764
              ||| ||    | | | |  | |   || ||   | |   | || |   |  || |||
Db        619 GAGGAGGAGGGGCTGGATGGTGAGGGGCTGGGAAAGGAGGAGGGGCTGGGAGCGGAGGTG 560

Qy        765 GAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAA 824
              | | | ||    | ||     |  |    |||   |||  | || ||  | |  |   |
Db        559 GGAGGAGGGGCTGGCAGAGGAGAAGGGGCTGAGGAGGTACTGGAAAAGAAAGAGGAGCAG 500

Qy        825 CAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGA 859
               |||    ||| ||   |  |||| | |||   ||
Db        499 GAGCTGGAGGAAGACGTGGAGGAGGAGCTGGAGGA 465

RESULT 11
US-09-991-936-317/c
; Sequence 317, Application US/09991936
; Publication No. US20030073827A1
; GENERAL INFORMATION:
;  APPLICANT: Brandt, Kevin S.
;  APPLICANT:  Gaines, Patrick J.
;  APPLICANT:  Stinchcomb, Dan T.
;  APPLICANT:  Wisnewski, Nancy
;  TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
;  FILE REFERENCE: FC-6-C1
;  CURRENT APPLICATION NUMBER: US/09/991,936
;  CURRENT FILING DATE:  2001-11-21
;  PRIOR APPLICATION NUMBER: US/09/543,668
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: 60/128,704
;  PRIOR FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 1959
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 317
;   LENGTH: 500
;   TYPE: DNA
;   ORGANISM: Ctenocephalides felis
US-09-991-936-317

  Query Match              3.8%;  Score 48.2;  DB 10;  Length 500;
  Best Local Similarity   48.4%;  Pred. No. 0.00045;
  Matches  119;  Conservative    0;  Mismatches  127;  Indels    0;  Gaps    0;

Qy        566 AGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGA 625
              | | || ||||     | |  |    | |  || ||  | || || ||  | || |||||
Db        441 ATGGTTATTTTTGTAAAGGGCTTGCCAAGCAATTTCAAAACCTATTTGCATAGTTAGTGA 382

Qy        626 CACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGAC 685
               |  || ||     | || ||  | |||||   ||    ||||| ||          ||
Db        381 TATCCGCAGGAACNCAGATATAAAATGGTTTATTGAAAAATATGGTGCTAAAGTTATAAC 322

Qy        686 GGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGG 745
                |  |  ||          |    |  ||| |    || || |||   || ||   |||
Db        321 NATTAGAATTAATTGCAGTAAATGCATTCGANAATNTCGAGGTTGGAAATTTACNGAAGG 262

Qy        746 GGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCAT 805
               || || ||||| ||  |  |||||||   |  | || |  |   |||  || |  |   |
Db        261 TGTTGATGATGTTGCNTNTGAATGTGATTTANATAATTATGAAAACTGGGATTTTGNTCT 202

Qy        806 CGAGAA 811
               |  ||
Db        201 TGTTAA 196

RESULT 12
US-10-271-416-6
; Sequence 6, Application US/10271416
; Publication No. US20040043021A1
; GENERAL INFORMATION:
;  APPLICANT: Keith, Tim
;  APPLICANT:  Little, Randall D.
;  APPLICANT:  Van Eerdewegh, Paul
;  APPLICANT:  Dupuis, Josee
;  APPLICANT:  Del Mastro, Richard G.
;  APPLICANT:  Allen, Kristina
;  TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
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  TITLE OF INVENTION:  RELATING TO RESPIRATORY DISEASES AND OBESITY
  FILE REFERENCE: 2976-4045
  CURRENT APPLICATION NUMBER: US/10/271,416
  CURRENT FILING DATE:  2002-10-11
  PRIOR APPLICATION NUMBER: 60/328,424
  PRIOR FILING DATE: 2001-10-11
  NUMBER OF SEQ ID NOS: 9
  SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 6
   LENGTH: 22693
   TYPE: DNA
   ORGANISM: Homo sapien
S-10-271-416-6

 Query Match             3.7%;  Score 47.4;  DB 12;  Length 22693;
 Best Local Similarity   53.5%;  Pred. No. 0.0021;
 Matches   99;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

 y          256 GGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGGCCCCGCTGG 315
                ||   | |||||  ||||  |||      || ||| |||| || |  | ||   ||||||
 b        21406 GGAGAGAAGAAGGATCAGGCTCAAAGTGTGCCAGGGGTGGGGGCGGAGGGAGGCGCTGG 21465

 y          316 GAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGAAGGACTTCG 375
                   | |||    ||    | | |||| |    |||| | ||   |        | | ||
 b        21466 CCTGTGCCAGCGGGGATCTGCGGCTGATGTATGGCATGTGGGCTGGAAAGCTGCCATCA 21525

 y          376 TGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCCGGCTCTCTG 435
                |  || ||  || | ||   | ||   ||| |  || | |||||| |||  |||||  ||
 b        21526 TAGCCCAGTAGCGGAAGGAAAAACGGAGAGGTCCTGGCGGTGCTGGCCTGAGGCTCAGTG 21585

 y          436 GTCCA 440
                   ||
 b        21586 AGTCA 21590

ESULT 13
S-10-425-114-831
 Sequence 831, Application US/10425114
 Publication No. US20040034888A1
 GENERAL INFORMATION:
  APPLICANT: Liu, Jingdong
  APPLICANT:  Zhou, Yihua
  APPLICANT:  Kovalic, David K.
  APPLICANT:  Screen, Steven E
  APPLICANT:  Tabaska, Jack E
  APPLICANT:  Cao, Yongwei
  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
  FILE REFERENCE: 38-21(53313)B
  CURRENT APPLICATION NUMBER: US/10/425,114
  CURRENT FILING DATE:  2003-04-28
  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 831
;   LENGTH: 830
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 700093880_FLI
S-10-425-114-831

  Query Match             3.4%;  Score 43.6;  DB 12;  Length 830;
  Best Local Similarity   43.8%;  Pred. No. 0.012;
  Matches  190;  Conservative    0;  Mismatches  244;  Indels    0;  Gaps    0;

Qy          303 ATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCC 362
                |||||   |  |      | || |   | |   ||| || |    ||      |    ||
Db           71 ATGGCGGAGGCGCACCCGGACCTGGTCCGGTCGCTGGTGGTGTCGGGGTCCGTGGTGGCC 130

Qy          363 GGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTC 422
                  ||  |||| | | | |||||||  || |    |  | || |   |    |  || |
Db          131 ATGACCGACTCCCTCAGCGAGGCGACGCTGGAGGGGATCGGCGTGAAGTCGTCGGCCGAG 190

Qy          423 CTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAG 482
                || | |||  | |   |  ||||||  |   | || | |   |  | |   | || || |
Db          191 CTGCTGCTGCCGGAGTCCGTCAAGGGGCTCAAGGCGCTGCTCTCCGTCGCTACCTACCGG 250

Qy          483 AGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGA 542
                |  |||  |  | ||  |  |  | |   || ||  |   |||  ||| ||  |    |
Db          251 AAGCTCTGGTTCCCCGACCGCCTCCACAGGGACTACCTCGAGGTGATGTTCACCAACCGC 310

Qy          543 GAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCC 602
                 |||||| | || ||        ||| ||  |   ||| || |  |  |    | |  ||
Db          311 AAGGAGAGAGGCGAGCTGCTGGAAGGTTTGGTGGTCAGCAACAAAGACGCCACCGTGCCC 370

Qy          603 CAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAG 662
                   |    |  |    |           || ||| |   |||| |   |        |||
Db          371 GTCCTGCCCCAGAAAATACTCCTGTTGTGGGGAGAGAACGACAACATCTTCAACATCGAG 430

Qy          663 GCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCAG 722
                  |     | |  |||   ||  | || |||      ||  |  |||||||  |    ||
Db          431 CTCGCCAAGACAATGAAAGAGCAGCTCGGCGAGAAGACGACGCTGCAGAGCATAAGCAAG 490

Qy          723 CGGGGCTGGGTGTT 736
                   |||    || |
Db          491 GCCGGCCACCTGGT 504

RESULT 14
US-10-184-644-346
; Sequence 346, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C227
;  CURRENT APPLICATION NUMBER: US/10/184,644
;  CURRENT FILING DATE:  2002-06-28
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 346
;   LENGTH: 671
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-184-644-346

  Query Match             3.3%;  Score 42.2;  DB 14;  Length 671;
  Best Local Similarity   6.9%;  Pred. No. 0.03;
  Matches   38;  Conservative  202;  Mismatches  305;  Indels    2;  Gaps    1;

Qy          477 TTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGC 536
                :::    ::     | :      :|:: |   :: :::       |:|:: : ::   |:
Db           66 DKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDEDRGV 125

Qy          537 TGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGC 596
                  :  : |  |:::: : ::::  :: :  :: |   :  :: : :    : :   :: :
Db          126 MAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPS 185

Qy          597 ATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTT 656
                    : : : :  |:: : |  ::|  :| :    | : :::       :: |: :| :
Db          186 EEENSESSSESEKTSDQDFTPEKKAAVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKP 245

Qy          657 CGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGA 716
                  : : ::    ::::::::::::: :  :|     :   : : :: :  :  : ::::
Db          246 EPVAMARSASSSSSSSSSSDSDVSVKKPPRGRKPAEKPLPKRGRKPKPERPPSSSSSDS 305
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Qy        717 CAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCTG 776
                : ::  :    ::  :        ::      :  :   :  :  :: : : |    |
Db        306 DSDEVDRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERG 365

Qy        777 GACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAG 836
              :     :  : ::   :::  :|:|    :: :    |   :  :: |    :::|  |:
Db        366 SGGSSGDELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTEPAR 425

Qy        837 GAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGG 896
              : |   : ::::      |: : :  |:: :   :::: : ::   ::     : :   :
Db        426 KPG--QKEKRVRPEEKQQAKPVKVERTRKRSEGFSMDRKVEKKKEPSVEEKLQKLHSEIK 483

Qy        897 AGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCC 956
                 :::: ::::|       |   : :    :  ::: | :: ::    :::  :   ::
Db        484 FALKVDSPDVKRCLNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMEKAAEVY 543

Qy        957 CGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGA 1016
               : ::   |     : :: :| : :  |  :  |           :| :: :|: :  :
Db        544 TRLKSRVLGPKIEAVQKVNKAGMEKEKAEEKLAGEELAGEEAPQEKAEDKPSTDLSAPVN 603

Qy       1017 TATTGGG 1023
                 |: :
Db        604 GEATSQK 610

RESULT 15
US-10-184-634-346
; Sequence 346, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C217
;  CURRENT APPLICATION NUMBER: US/10/184,634
;  CURRENT FILING DATE:  2002-06-28
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 346
;   LENGTH: 671
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-184-634-346

  Query Match              3.3%;  Score 42.2;  DB 14;  Length 671;
  Best Local Similarity   6.9%;  Pred. No. 0.03;
  Matches   38;  Conservative  202;  Mismatches  305;  Indels    2;  Gaps    1;

Qy        477 TTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGC 536
              :::    ::     | :      :|:: |   :: :::       |:|:: : ::   |:
Db         66 DKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDEDRGV 125

Qy        537 TGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGC 596
                :  : |  |:::: : ::::  :: :  :: |   :  :: : :    : :   :: :
Db        126 MAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPS 185

Qy        597 ATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTT 656
                  : : : :  |:: : |  ::|  :| :    | : :::       :: |: :| :
Db        186 EEENSESSSESEKTSDQDFTPEKKAAVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKP 245

Qy        657 CGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGA 716
                : : ::    ::::::::::::: :  :|     :   : : :: :  :  : ::::
Db        246 EPVAMARSASSSSSSSSSDSDVSVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDS 305
```

```
Qy        717 CAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCTG 776
                : ::  :    ::  :        ::      :  :   :  :  :: : : |    |
Db        306 DSDEVDRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERG 365

Qy        777 GACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAG 836
              :     :  : ::   :::  :|:|    :: :    |   :  :: |    :::|  |:
Db        366 SGGSSGDELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTEPAR 425

Qy        837 GAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGG 896
              : |   : ::::      |: : :  |:: :   :::: : ::   ::     : :   :
Db        426 KPG--QKEKRVRPEEKQQAKPVKVERTRKRSEGFSMDRKVEKKKEPSVEEKLQKLHSEIK 483

Qy        897 AGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCC 956
                 :::: ::::|       |   : :    :  ::: | :: ::    :::  :   ::
Db        484 FALKVDSPDVKRCLNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMEKAAEVY 543

Qy        957 CGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGA 1016
               : ::   |     : :: :| : :  |  :  |           :| :: :|: :  :
Db        544 TRLKSRVLGPKIEAVQKVNKAGMEKEKAEEKLAGEELAGEEAPQEKAEDKPSTDLSAPVN 603

Qy       1017 TATTGGG 1023
                 |: :
Db        604 GEATSQK 610
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Job time : 307.609 secs
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                Copyright (c) 1993 - 2004  Compugen Ltd.

M nucleic - nucleic search, using sw model

un on:         March 10, 2004, 09:19:42 ; Search time 58.4979 Seconds
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'itle:         US-10-084-817-1
'erfect score: 1281
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;coring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

;earched:      682709 seqs, 277475446 residues

'otal number of hits satisfying chosen parameters:      1365418

linimum DB seq length: 0
laximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries

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                6:  /cgn2_6/ptodata/2/ina/backfiles1.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                 SUMMARIES
                     %
:esult              Query
  No.     Score     Match Length DB  ID                            Description
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     1    317.2     24.8     419  4  US-09-621-976-3203            Sequence 3203, Ap
c    2       49      3.8    7218  1  US-08-232-463-14              Sequence 14, Appl
c    3     39.8      3.1 4403765  3   US-09-103-840A-2              Sequence 2, Appli
c    4     39.8      3.1 4411529  3   US-09-103-840A-1              Sequence 1, Appli
     5     39.6      3.1    1536  4  US-09-252-991A-7459           Sequence 7459, Ap
c    6     39.6      3.1    1665  4  US-09-252-991A-7242           Sequence 7242, Ap
     7     39.6      3.1    1713  4  US-09-252-991A-7383           Sequence 7383, Ap
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     9     38.8      3.0    1644  4  US-09-252-991A-6420           Sequence 6420, Ap
    10     38.8      3.0    2088  4  US-09-252-991A-6339           Sequence 6339, Ap
c   11     38.8      3.0    2202  4  US-09-252-991A-6131           Sequence 6131, Ap
    12     37.2      2.9    1437  4  US-09-647-224A-9              Sequence 9, Appli
c   13       37      2.9    1036  4  US-09-072-596-304             Sequence 304, App
c   14       37      2.9    1036  4  US-09-072-967-309             Sequence 309, App
c   15     36.4      2.8     831  4  US-09-252-991A-532            Sequence 532, App
    16     36.4      2.8    2478  4  US-09-252-991A-592            Sequence 592, App
c   17       36      2.8    4078  4  US-09-016-434-1120            Sequence 1120, Ap
c   18     35.6      2.8     314  4  US-09-916-510A-8              Sequence 8, Appli
c   19     35.6      2.8     430  4  US-09-621-976-16656           Sequence 16656, A
    20     35.6      2.8    2291  2  US-08-476-062A-53             Sequence 53, Appl
    21     35.6      2.8    2310  2  US-08-476-062A-41             Sequence 41, Appl
    22     35.6      2.8    2310  5  PCT-US96-01314-41             Sequence 41, Appl
    23     35.6      2.8    2405  3  US-08-549-846-3               Sequence 3, Appli
    24     35.6      2.8    2776  4  US-09-023-655-1146            Sequence 1146, Ap
c   25     35.2      2.7    1305  4  US-09-252-991A-5951           Sequence 5951, Ap
    26       35      2.7    2511  4  US-09-489-039A-530            Sequence 530, App
c   27     34.8      2.7    1073  4  US-09-072-596-322             Sequence 322, App
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c   28     34.8      2.7    1073  4  US-09-072-967-327             Sequence 327, App
    29     34.8      2.7 4403765  3   US-09-103-840A-2              Sequence 2, Appli
    30     34.8      2.7 4411529  3   US-09-103-840A-1              Sequence 1, Appli
    31     34.6      2.7    1203  4  US-09-489-039A-5574           Sequence 5574, Ap
    32     34.6      2.7    4046  1  US-07-793-961A-1              Sequence 1, Appli
    33     34.6      2.7    4046  1  US-08-240-357-1               Sequence 1, Appli
    34     34.4      2.7     888  4  US-08-765-907A-2              Sequence 2, Appli
    35     34.4      2.7     996  4  US-09-252-991A-9594           Sequence 9594, Ap
    36     34.4      2.7    1014  4  US-09-252-991A-11274          Sequence 11274, A
c   37     34.4      2.7    1785  4  US-09-252-991A-9701           Sequence 9701, Ap
c   38     34.4      2.7    2100  4  US-09-252-991A-9660           Sequence 9660, Ap
c   39     34.4      2.7    2888  4  US-08-765-907A-1              Sequence 1, Appli
    40     34.4      2.7    4131  3  US-08-726-214-11              Sequence 11, Appl
c   41     34.2      2.7     735  4  US-09-252-991A-14239          Sequence 14239, A
    42     34.2      2.7     864  4  US-09-252-991A-10932          Sequence 10932, A
    43     34.2      2.7    1410  4  US-09-252-991A-14025          Sequence 14025, A
c   44     34.2      2.7    2211  4  US-09-252-991A-11256          Sequence 11256, A
    45     34.2      2.7    2289  4  US-09-252-991A-10995          Sequence 10995, A

                                 ALIGNMENTS

RESULT 1
US-09-621-976-3203
; Sequence 3203, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 3203
;   LENGTH: 419
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 75..380
US-09-621-976-3203

  Query Match             24.8%;  Score 317.2;  DB 4;  Length 419;
  Best Local Similarity   85.6%;  Pred. No. 2.8e-76;
  Matches  416;  Conservative    0;  Mismatches    3;  Indels   67;  Gaps    3;

Qy        229 CATTCCGCGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGA 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CATTCCGCGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGA 60

Qy        289 GGCGTGGCGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCG 348
              |||||||||||||||||||||     ||||||||||||||||||||||||||||||||||
Db         61 GGCGTGGCGGCCCCATGGCCC--GCTGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCG 118

Qy        349 GCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTG 408
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        119 GCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAG-------------- 164

Qy        409 ATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATG 468
                                                                ||||||||||
Db        165 --------------------------------------------------CAGGAGCATG 174

Qy        469 GCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACA 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 GCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACA 234

Qy        529 TGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTG 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 TGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTG 294
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Qy         589 TGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCC 648
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         295 TGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCC 354

Qy         649 AGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGC 708
               |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db         355 AGTGGTTTCGGGAGGCCTATGGGG-CGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGC 413

Qy         709 AGAGCC 714
               ||||||
Db         414 AGAGCC 419

RESULT 2
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             3.8%;  Score 49;  DB 1;  Length 7218;
  Best Local Similarity   3.3%;  Pred. No. 0.002;
  Matches   13;  Conservative  218;  Mismatches  158;  Indels    0;  Gaps    0;

Qy         651 TGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAG 710
               ||||   ::::::   : ::::  : :: : ::: ::   : :  : :: :  :::: ::
Db        1440 TGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1381

Qy         711 AGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGT 770
               ::  :: :: :: ::::  ::: :    : : ::::: ::: :: :  :::  :::: :
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Db        1380 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1321

Qy         771 GGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGC 830
               ::   ::: ::    :::::    ::  :::  :  :::::  : ::::  ::: :: :
Db        1320 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1261

Qy         831 CTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGT 890
                 ::::::: ::  ::::::   :: ::::   :   :    :::    ::  :  :::
Db        1260 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1201

Qy         891 TCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATGGGGGT 950
                  ::::: :::  ::::   :  :::: ::::: ::::  ::    : :::: :::::
Db        1200 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1141

Qy         951 GTCCCCCGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTT 1010
               :      ::    ::  :::: :::::: ::: ::::::::   :::    :::::::
Db        1140 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1081

Qy        1011 GGTGGATATTGGGCAAGGCAGGAAACCTC 1039
               :: ::: :  ::: |  ||| |   ||||
Db        1080 RRRRRRRRRRRRRRATCGCAAGCTCCCTC 1052

RESULT 3
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

  Query Match             3.1%;  Score 39.8;  DB 3;  Length 4403765;
  Best Local Similarity   49.8%;  Pred. No. 5.9;
  Matches  127;  Conservative    0;  Mismatches  127;  Indels    1;  Gaps    1;

Qy         121 GTTTGGACATGAGCTGAGGGCACGGTCGCGGGCGGTCAGCCCTGTTCGCAGCTACGGCGA 180
               ||| |   | |||| | | |    | ||  ||| |  | |    | |   |    | ||||
Db     2904687 GTTCGCCAAGGAGCGGCGTGAGGAGGCGTTGGAGACCGGTAAGGATGCGATGGCCCGCGA 2904628

Qy         181 GGAGGGGCGCGATTGTTCCTTGTTGCCGCTCCGCTTAGTGGCCGCGTCCATTCCGCGCGG 240
               || | | |||| | |      ||||| || |    |    |  | ||||||  || ||||
Db     2904627 GGTGCGCCGCGGTGGACTTCCGTTGCAGCGCTTGGTCAATGGTGAGTCCATGGCG-GCGG 2904569

Qy         241 TGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCC 300
               || ||||      |   || |  || ||||||||       | ||| |   |||  || |
Db     2904568 TGGCCCGCGAGCTGCACTACGCGGACGTGTCAGCACTCTATACCGCCATCGGTGAGGGGC 2904509

Qy         301 CCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAAT 360
                | || |  ||      | ||  | |||| || |      | || |||| |      |
Db     2904508 ACGTGTCGGCGAAACACGTCGTGCAGCGGTTGTTGGCCGAGCTCGGCGGTATCGACCAGG 2904449

Qy         361 CCGGGAAGGACTTCG 375
               | |   ||||  |||
Db     2904448 CGGAAGAGGAACTCG 2904434
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RESULT 4
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match              3.1%;  Score 39.8;  DB 3;  Length 4411529;
  Best Local Similarity   49.8%;  Pred. No. 5.9;
  Matches  127;  Conservative    0;  Mismatches  127;  Indels    1;  Gaps    1;

Qy        121 GTTTGGACATGAGCTGAGGGCACGGTCGCGGGCGGTCAGCCCTGTTCGCAGCTACGGCGA 180
              ||| |   | |||| | | |    | ||  || |  | |    | |   |    | ||||
Db    2908580 GTTCGCCAAGGAGCGGCGTGAGGAGGCGTTGGAGACCGGTAAGGATGCGATGGCCCGCGA 2908521

Qy        181 GGAGGGGCGCGATTGTTCCTTGTTGCCGCTCCGCTTAGTGGCCGCGTCCATTCCGCGCGG 240
              || | | |||| | |      ||||| || |    |    |  | ||||||  || ||||
Db    2908520 GGTGCGCCGCGGTGGACTTCCGTTGCAGCGCTTGGTCAATGGTGAGTCCATGGCG-GCGG 2908462

Qy        241 TGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCC 300
              || ||||      |   || |  || ||||||||       | ||| |   |||  || |
Db    2908461 TGGCCCGCGAGCTGCACTACGCGGACGTGTCAGCACTCTATACCGCCATCGGTGAGGGGC 2908402

Qy        301 CCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAAT 360
               | || |  ||      | ||  | |||| || |      | || |||| |      |
Db    2908401 ACGTGTCGGCGAAACACGTCGTGCAGCGGTTGTTGGCCGAGCTCGGCGGTATCGACCAGG 2908342

Qy        361 CCGGGAAGGACTTCG 375
              | |   ||||  |||
Db    2908341 CGGAAGAGGAACTCG 2908327

RESULT 5
US-09-252-991A-7459
; Sequence 7459, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7459
;   LENGTH: 1536
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7459

  Query Match              3.1%;  Score 39.6;  DB 4;  Length 1536;
  Best Local Similarity   49.1%;  Pred. No. 0.4;
  Matches  105;  Conservative    0;  Mismatches  109;  Indels    0;  Gaps    0;

Qy        307 CCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGA 366
              |||    ||  | || |  | |     |  ||||| || |||||   |     | ||| |
Db        830 CCCGCGCGGCGGTCGACGAGTGCGATTTCGTGCTGGTCGGCGGCCTCACCGGTTGCGGCA 889

Qy        367 AGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCC 426
              ||  |   |||| || ||||||| | | ||| || |     || | |   ||   ||  |
Db        890 AGACCGAGGTGATCGCGGCGCTGGACAACAGCCTCGATCTCGAAGGCCACGCCAACCATC 949

Qy        427 GGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGAC 486
              |   |||  |      |  |  |       | |||  |       |  ||||| |||  |
Db        950 GCGGCTCCAGCTTTGGCCGGCGAGCCACGCCGCAGCCGGCGCAGATCGACTTCGAGAACC 1009

Qy        487 TCCTGGACACCAGCACCTACAAGGAGGCCTTTCG 520
               ||||| || |  || |   ||| ||     |||
Db       1010 GCCTGGCCATCGACATCCTGAAGAAGCGTCATCG 1043

RESULT 6
US-09-252-991A-7242/c
; Sequence 7242, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7242
;   LENGTH: 1665
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7242

  Query Match              3.1%;  Score 39.6;  DB 4;  Length 1665;
  Best Local Similarity   49.1%;  Pred. No. 0.41;
  Matches  105;  Conservative    0;  Mismatches  109;  Indels    0;  Gaps    0;

Qy        307 CCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGA 366
              |||    ||  | || |  | |     |  ||||| || |||||   |     | ||| |
Db       1064 CCCGCGCGGCGGTCGACGAGTGCGATTTCGTGCTGGTCGGCGGCCTCACCGGTTGCGGCA 1005

Qy        367 AGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCC 426
              ||  |   |||| || ||||||| | | ||| || |     || | |   ||   ||  |
Db       1004 AGACCGAGGTGATCGCGGCGCTGGACAACAGCCTCGATCTCGAAGGCCACGCCAACCATC 945

Qy        427 GGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGAC 486
              |   |||  |      |  |  |       | |||  |       |  ||||| |||  |
Db        944 GCGGCTCCAGCTTTGGCCGGCGAGCCACGCCGCAGCCGGCGCAGATCGACTTCGAGAACC 885

Qy        487 TCCTGGACACCAGCACCTACAAGGAGGCCTTTCG 520
               ||||| || |  || |   ||| ||     |||
Db        884 GCCTGGCCATCGACATCCTGAAGAAGCGTCATCG 851

RESULT 7
US-09-252-991A-7383
; Sequence 7383, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7383
;   LENGTH: 1713
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7383

  Query Match              3.1%;  Score 39.6;  DB 4;  Length 1713;
  Best Local Similarity   49.1%;  Pred. No. 0.41;
  Matches  105;  Conservative    0;  Mismatches  109;  Indels    0;  Gaps    0;

Qy        307 CCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGA 366
              |||    ||  | || |  | |     |  ||||| || |||||   |     | ||| |
Db        765 CCCGCGCGGCGGTCGACGAGTGCGATTTCGTGCTGGTCGGCGGCCTCACCGGTTGCGGCA 824

Qy        367 AGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCC 426
              ||  |   |||| || ||||||| | | ||| || |     || | |   ||   ||  |
Db        825 AGACCGAGGTGATCGCGGCGCTGGACAACAGCCTCGATCTCGAAGGCCACGCCAACCATC 884

Qy        427 GGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGAC 486
              |   |||  |      |  |  |       | |||  |       |  ||||| |||  |
Db        885 GCGGCTCCAGCTTTGGCCGGCGAGCCACGCCGCAGCCGGCGCAGATCGACTTCGAGAACC 944

Qy        487 TCCTGGACACCAGCACCTACAAGGAGGCCTTTCG 520
               ||||| || |  || |   ||| ||     |||
Db        945 GCCTGGCCATCGACATCCTGAAGAAGCGTCATCG 978


RESULT 8
US-09-621-976-2574/c
; Sequence 2574, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 2574
;   LENGTH: 834
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 497..826
US-09-621-976-2574

  Query Match              3.1%;  Score 39.2;  DB 4;  Length 834;
  Best Local Similarity   20.9%;  Pred. No. 0.41;
  Matches   56;  Conservative   92;  Mismatches  120;  Indels    0;  Gaps    0;

Qy        265 AAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGGCCCCGCTGGGAGGCGCCC 324
              | | ||  |||   || |  | | ||  || |       ||| |     |  |||: |
Db        277 AGGAGTGCGCTGGCGGGACGGTGGGGTCTGCCTTGGGGTTGGACTTAGGGTTAGGSWCTA 218

Qy        325 CGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGG 384
               |  ||      || |    |||     ::|:::  | :  :::|: : : ||| ::: :
Db        217 TGTCGCCCCCGGTGGTCACGAGCATGKSSMGSMWGSCKSMWMWKGMKYSMYTGAWYRRYK 158

Qy        385 CGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCA 444
               :::|     |::   : :   :| :::: : :::|:  : ::|:  :  : ::  ::::
Db        157 GRYWGWYTSWCRKGKSYCSCWKKGKYSYSMRGSYKGKWWWKSRGYRKYRSRAWSRCYKMW 98

Qy        445 AGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCT 504
              : ::::::::: ::: :  .: :::| ::  :| |: : | :||   : : ::|:: :|:

Db         97 MASWRSWSYMYMYWSSKYCASGWSKCAWSKGMTMCYYSKGYYTCRSMSYYKYSASYGSCW 38

Qy        505 ACAAGGAGGCCTTTCGGAAGGACATGAT 532
               |  ::  ::: :: ::   : ::: :|
Db         37 CCYGKSYCKSSMYYASSYCCSGSWWMMT 10


RESULT 9
US-09-252-991A-6420
; Sequence 6420, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 6420
;   LENGTH: 1644
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6420

  Query Match              3.0%;  Score 38.8;  DB 4;  Length 1644;
  Best Local Similarity   53.2%;  Pred. No. 0.67;
  Matches   82;  Conservative    0;  Mismatches   72;  Indels    0;  Gaps    0;

Qy        295 GCGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGA 354
              | | |  ||  | |||| |||| |||| | ||| | | |   ||| |  ||    ||| |
Db        581 GGGTCGGCAACGTCCCGGTGGGCGGCGACGCGCCGATCGCCGTGCAGAGCATGACCAACA 640

Qy        355 GGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCT 414
                 |  || |  | | |   |  ||||  |||| |    || | || | || ||  | |
Db        641 CCGAGACCTGCGACGTCGCTGCCACCGTCGCGCAGATCCGCCGCCTGGAAGATGCCGGCG 700

Qy        415 GTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGA 448
                |   || | ||| | || |  ||   || |||
Db        701 CGGACATCGTGCGGGTTTCCGTCCCCGACATGGA 734


RESULT 10
US-09-252-991A-6339
; Sequence 6339, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 6339
;   LENGTH: 2088
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6339

  Query Match              3.0%;  Score 38.8;  DB 4;  Length 2088;
  Best Local Similarity   53.2%;  Pred. No. 0.73;
  Matches   82;  Conservative    0;  Mismatches   72;  Indels    0;  Gaps    0;

Qy        295 GCGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGA 354
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               | | |  ||  | |||| |||| |||| | ||| | | |   ||| |  ||    ||| |
b           39 GGGTCGGCAACGTCCCGGTGGGCGGCGACGCGCCGATCGCCGTGCAGAGCATGACCAACA 98

y          355 GGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCT 414
                  |  || |  | | |   |  ||||  |||| |    || | || | || ||  | |
b           99 CCGAGACCTGCGACGTCGCTGCCACCGTCGCGCAGATCCGCCGCCTGGAAGATGCCGGCG 158

y          415 GTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGA 448
                 |   || | ||| | || |  ||   || |||
b          159 CGGACATCGTGCGGGTTTCCGTCCCCGACATGGA 192

ESULT 11
S-09-252-991A-6131/c
; Sequence 6131, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 6131
;   LENGTH: 2202
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
S-09-252-991A-6131

  Query Match             3.0%;  Score 38.8;  DB 4;  Length 2202;
  Best Local Similarity   53.2%;  Pred. No. 0.75;
  Matches   82;  Conservative    0;  Mismatches   72;  Indels    0;  Gaps    0;

y          295 GCGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGA 354
               | | |  ||  | |||| |||| |||| | ||| | | |   ||| |  ||    ||| |
b         2081 GGGTCGGCAACGTCCCGGTGGGCGGCGACGCGCCGATCGCCGTGCAGAGCATGACCAACA 2022

y          355 GGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCT 414
                  |  || |  | | |   |  ||||  |||| |    || | || | || ||  | |
Db        2021 CCGAGACCTGCGACGTCGCTGCCACCGTCGCGCAGATCCGCCGCCTGGAAGATGCCGGCG 1962

y          415 GTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGA 448
                 |   || | ||| | || |  ||   || |||
Db        1961 CGGACATCGTGCGGGTTTCCGTCCCCGACATGGA 1928

RESULT 12
US-09-647-224A-9
; Sequence 9, Application US/09647224A
; Patent No. 6482631
; GENERAL INFORMATION:
;  APPLICANT:  Cahoon, Rebecca E.
;  APPLICANT:  Falco, Saverio Carl
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Hitz, William D.
;  APPLICANT:  Maxwell, Carl A.
;  APPLICANT:  Rafalski, J. Antoni
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Vollmer, Steven J.
;  TITLE OF INVENTION: TRYPTOPHAN BIOSYNTHETIC ENZYMES
;  FILE REFERENCE: BB-1150-A
;  CURRENT APPLICATION NUMBER: US/09/647,224A
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 60/079,386
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: PCT/US99/06046
;  PRIOR FILING DATE: 1999-03-19
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
;   LENGTH: 1437
;   TYPE: DNA
;   ORGANISM: Zea mays
US-09-647-224A-9

  Query Match             2.9%;  Score 37.2;  DB 4;  Length 1437;
  Best Local Similarity   44.7%;  Pred. No. 1.7;
  Matches  144;  Conservative    0;  Mismatches  178;  Indels    0;  Gaps    0;

Qy         746 GGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCAT 805
               || |   || |  |||   | |     |||  ||| | | | | |  |    |||| ||
Db         363 GGAGATAGAGGAGGAGCTGGGAGCCCCCCTTAACATCCTAGAGAAGATCATTTGGGACAA 422

Qy         806 CGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTAT 865
                ||||   | | || |||   ||      || |||   | ||| |  ||||  |   |
Db         423 GGAGATTGAAGTAGCTGAGGGGCATGCTAAGAAGCCTCTTGAGGAGGTGATTCAGGCTGC 482

Qy         866 CCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGT 925
                         | |   |||  ||  |      | |   | |   ||||  |   | |
Db         483 AACGAAAGCCCCTCCTTCAAGAGACTTCTATGGCGCTTTAGAAGCTGCCTACAAGCGTAA 542

Qy         926 GGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGACAG 985
                ||| || ||      | ||  |  |||     | | |  |||||  | ||      |||
Db         543 TGGGGTGCCTGCATTGATTGCTGAGGTCAAGAAAGCATCCCCGAGTAGGGGTGTGCTCAG 602

Qy         986 GGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGGAGA 1045
               || |    |  || |||  |   ||| |  |  ||  | || | | | | |  |  |
Db         603 GGAGAACTTTAATCCTGTTGAAATTGCTCAAGCTTATGAAAAGAATGGAGCTGCATGTTT 662

Qy        1046 CCTCATTTTCTCCATGGGGAAG 1067
                  ||||||  |    | ||||
Db         663 GAGCATTTTGACAGATGAGAAG 684

RESULT 13
US-09-072-596-304/c
; Sequence 304, Application US/09072596
; Patent No. 6458366
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Dillon, Davin C.
;    APPLICANT:  Campos-Neto, Antonia
;    APPLICANT:  Houghton, Raymond
;    APPLICANT:  Vedvick, Thomas S.
;    APPLICANT:  Twardzik, Daniel R.
;    APPLICANT:  Lodes, Michael J.
;    APPLICANT:  Hendrickson, Ronald C.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR DIAGNOSIS OF    TUBERCULOSIS
;    NUMBER OF SEQUENCES:  350
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/072,596
;      FILING DATE:  05-MAY-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.417C9
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  304:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1036 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
US-09-072-596-304

  Query Match             2.9%;  Score 37;  DB 4;  Length 1036;
  Best Local Similarity   29.3%;  Pred. No. 1.7;
  Matches  118;  Conservative   55;  Mismatches  230;  Indels    0;  Gaps    0;

Qy         613 GGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAGGCCTATGGGG 672
               ||    :| |  | | |: |:|  |    || |       |:  |:|:|| :    |:||
Db         998 GGAGANYGNGGAAGAGAMMGMGKNTNRGNGAKAANRGNGWGWAMCSGRAGAMKVKNGKGG 939

Qy         673 CCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCAGCGGGGCTGGG 732
                 | |  | |   |::: :    |  | || :     | |:       ::  |||  |||
Db         938 GAGGGGGGGAAGGGKWMNRAMMGGGGGRGTNKAGAKGGGGSGMGRGWAWSGMGGGKMGGG 879

Qy         733 TGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACT 792
               ::| :|  :  | || | : ||   |      ::  |     : :: :  ||     : |
Db         878 WKTAMAANMGNGNGGGGNRNGAGWGTCKTAWTKWGNGMMNNRWTRWGWGGTTTTATAWKT 819

Qy         793 TTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAGAACC 852
                 :|: ||| | :| |  :   :  |   |  |   :: ||:|  | |  | | | | :
Db         818 GASASMGGGGGAGYGNGGGYGNARTTGGGMAGKANAAMSNGGMGWKGWANATTGGGNAKS 759

Qy         853 TGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTG 912
                 : :|   |  | :|     |   :|        |    :|:| | |||   :   |
Db         758 CMRGMGGGGTNGTTMGAGGNGGNWGKTSMGAGGGGGNGMKYARGGGGGAGNAASAAGCCY 699

Qy         913 CTGAGGTGGGGGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGT 972
                 ::   ::||| | | :  |    |   ||  |||| |:     |     ||   |
Db         698 GNKMTTARSGGGGGNGNSANAWGGGGGTTAACCGGGGAGKTTNAAGGGGKGGGGGAACMC 639

Qy         973 GAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGG 1015
               | |:|    |   |:||||     | |  :  || || :  |:
Db         638 GGGRASATAANNMGSGGGGGGGSNANTTCSGNGGAGTNSAAGS 596


RESULT 14
US-09-072-967-309/c
; Sequence 309, Application US/09072967
; Patent No. 6592877
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Dillon, Davin C.
;    APPLICANT:  Campos-Neto, Antonio
;    APPLICANT:  Houghton, Raymond
;    APPLICANT:  Vedvick, Thomas S.
;    APPLICANT:  Twardzik, Daniel R.
;    APPLICANT:  Lodes, Michael J.
;    APPLICANT:  Hendrickson, Ronald C.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
;    TITLE OF INVENTION:  AND DIAGNOSIS OF TUBERCULOSIS
;    NUMBER OF SEQUENCES:  355
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
```

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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/072,967
;      FILING DATE:  05-MAY-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.411C9
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  309:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1036 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
US-09-072-967-309

  Query Match             2.9%;  Score 37;  DB 4;  Length 1036;
  Best Local Similarity   29.3%;  Pred. No. 1.7;
  Matches  118;  Conservative   55;  Mismatches  230;  Indels    0;  Gaps    0;

Qy         613 GGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAGGCCTATGGGG 672
               ||    :| |  | | |: |:|  |    || |       |:  |:|:|| :    |:||
Db         998 GGAGANYGNGGAAGAGAMMGMGKNTNRGNGAKAANRGNGWGWAMCSGRAGAMKVKNGKGG 939

Qy         673 CCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCAGCGGGGCTGGG 732
                 | |  | |   |::: :    |  | || :     | |:       ::  |||  |||
Db         938 GAGGGGGGGAAGGGKWMNRAMMGGGGGRGTNKAGAKGGGGSGMGRGWAWSGMGGGKMGGG 879

Qy         733 TGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACT 792
               ::| :|  :  | || | : ||   |      ::  |     : :: :  ||     : |
Db         878 WKTAMAANMGNGNGGGGNRNGAGWGTCKTAWTKWGNGMMNNRWTRWGWGGTTTTATAWKT 819

Qy         793 TTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAGAACC 852
                 :|: ||| | :| |  :   :  |   |  |   :: ||:|  | |  | | | | :
Db         818 GASASMGGGGGAGYGNGGGYGNARTTGGGMAGKANAAMSNGGMGWKGWANATTGGGNAKS 759

Qy         853 TGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTG 912
                 : :|   |  | :|     |   :|        |    :|:| | |||   :   |
Db         758 CMRGMGGGGTNGTTMGAGGNGGNWGKTSMGAGGGGGNGMKYARGGGGGAGNAASAAGCCY 699

Qy         913 CTGAGGTGGGGGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGT 972
                 ::   ::||| | | :  |    |   ||  |||| |:     |     ||   |
Db         698 GNKMTTARSGGGGGNGNSANAWGGGGGTTAACCGGGGAGKTTNAAGGGGKGGGGGAACMC 639

Qy         973 GAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGG 1015
               | |:|    |   |:||||     | |  :  || || :  |:
Db         638 GGGRASATAANNMGSGGGGGGGSNANTTCSGNGGAGTNSAAGS 596


RESULT 15
US-09-252-991A-532/c
; Sequence 532, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 532
;   LENGTH: 831
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
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S-09-252-991A-532

  Query Match             2.8%;  Score 36.4;  DB 4;  Length 831;
  Best Local Similarity   53.5%;  Pred. No. 2.3;
  Matches   76;  Conservative    0;  Mismatches   66;  Indels    0;  Gaps    0;

y          689 CCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGT 748
               || | | ||  ||  |   | |||||||     | |||||  || | ||       ||
b          289 CCACTTCGTTTCGCCGATACCGAGCCGAGGCGCGTGGGGCCTGGCGATCTTCGACCGGCA 230

y          749 GGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGA 808
               |||          |     |||| | ||||||||||| ||||  | ||| | |||| |||
b          229 GGAGCGGTTGCTTTACCGCTGTGCCGTGGACAACTTCTGGGAGCTGGACAGCGTCACCGA 170

y          809 GAACCATGGAGTTGAACAGCGC 830
               |  | | |   | |  | || |
b          169 GCGCGAGGTGATCGGCCGGCAC 148

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Job time : 76.4979 secs
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          Copyright (c) 1993 - 2004  Compugen Ltd.

)M nucleic - nucleic search, using sw model

:un on:          March 10, 2004, 08:01:57 ; Search time 311.77 Seconds
                                            (without alignments)
                                            17454.974 Million cell updates/sec

'itle:           US-10-084-817-1
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:coring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

;earched:        3373863 seqs, 2124099041 residues

'otal number of hits satisfying chosen parameters:      6747726

linimum DB seq length: 0
laximum DB seq length: 2000000000

'ost-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

)atabase :        N_Geneseq_29Jan04:*
                 1:   geneseqn1980s:*
                 2:   geneseqn1990s:*
                 3:   geneseqn2000s:*
                 4:   geneseqn2001as:*
                 5:   geneseqn2001bs:*
                 6:   geneseqn2002s:*
                 7:   geneseqn2003as:*
                 8:   geneseqn2003bs:*
                 9:   geneseqn2003cs:*
                 10:   geneseqn2004s:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                   SUMMARIES
                      %
:esult             Query
  No.    Score    Match Length DB  ID                          Description
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     1   1255.8    98.0   1308  3  AAF21733                    Aaf21733 Human bre
     2    459.2    35.8    465  3  AAC02135                    Aac02135 Human sec
     3    398.6    31.1    475  8  ACH36439                    Ach36439 Human end
     4    394.2    30.8    407  8  ACH29232                    Ach29232 Human adu
     5    292.6    22.8    337  2  AAT23873                    Aat23873 Human gen
 c   6      125     9.8    502  4  AAL20639                    Aal20639 Human bre
     7       82     6.4    570  4  ABL30119                    Abl30119 Drosophil
 c   8     76.4     6.0    568  4  AAL11749                    Aal11749 Human bre
 c   9     60.8     4.7   2673  4  ABL30118                    Abl30118 Drosophil
 c  10     60.8     4.7   3406  4  ABL30184                    Abl30184 Drosophil
    11       60     4.7     60  6  ABN35477                    Abn35477 Human spl
    12     59.4     4.6   2000  7  ADA71938                    Ada71938 Rice gene
 c  13     56.8     4.4    467  9  ADB51434                    Adb51434 Primary r
    14       51     4.0   2100  7  ACA37843                    Aca37843 Prokaryot
 c  15     48.8     3.8    500  3  AAC93822                    Aac93822 Cat flea
 c  16     43.2     3.4   3704  4  ABL30114                    Abl30114 Drosophil
    17     39.8     3.1   2373  7  ACA40692                    Aca40692 Prokaryot
    18     39.8     3.1   2379  7  ACA38426                    Aca38426 Prokaryot
 c  19     39.8     3.1  80557  6  ABX09142                    Abx09142 Mycobacte
 c  20     39.8     3.1 110000  4  AAI99682_28                 Continuation (29 o
 c  21     39.8     3.1 110000  4  AAI99682_29                 Continuation (30 o
 c  22     39.8     3.1 110000  4  AAI99683_28                 Continuation (29 o
 c  23     39.8     3.1 110000  4  AAI99683_29                 Continuation (30 o
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    24     39.6     3.1   1110  7  ACA42257                    Aca42257 Prokaryot
    25       39     3.0    231  6  ABA04108                    Aba04108 Human lip
    26       39     3.0    249  6  ABA04112                    Aba04112 Human lip
 c  27     37.8     3.0   1337  2  AAZ17263                    Aaz17263 Human gen
    28     37.6     2.9   8212  6  ABI99884                    Abi99884 Mouse isc
    29     37.2     2.9   1116  7  ACA42498                    Aca42498 Prokaryot
    30     37.2     2.9   1437  2  AAZ22859                    Aaz22859 Maize ind
 c  31     37.2     2.9   1534  1  AAN71319                    Aan71319 Sequence
 c  32       37     2.9   1036  2  AAZ19209                    Aaz19209 M. tuberc
 c  33       37     2.9   1036  2  AAZ19421                    Aaz19421 M. tuberc
    34     36.6     2.9   6502  5  AAF98718                    Aaf98718 Human lat
    35     36.6     2.9   7319  6  AAS94894                    Aas94894 Human DNA
    36     36.4     2.8   1035  3  AAA51616                    Aaa51616 HIV gp41
 c  37     36.4     2.8   2000  7  ADA71938                    Ada71938 Rice gene
    38     36.4     2.8   2466  3  AAA51614                    Aaa51614 HIV gp160
    39     36.4     2.8   2547  3  AAA51615                    Aaa51615 HIV gp160
    40     36.4     2.8   2550  6  AAL44550                    Aal44550 HIV-1 env
    41     36.4     2.8   2550  6  ABL39955                    Abl39955 Synthetic
 c  42     36.2     2.8    536  9  ADB68842                    Adb68842 Minority
 c  43       36     2.8    575  4  AAI29394                    Aai29394 Colon tum
 c  44       36     2.8    575  7  ABZ33580                    Abz33580 Human col
 c  45       36     2.8   4078  7  ACA56522                    Aca56522 Human sig

                                  ALIGNMENTS


RESULT 1
AAF21733
ID   AAF21733 standard; DNA; 1308 BP.
XX
AC   AAF21733;
XX
DT   27-MAR-2001  (first entry)
XX
DE   Human breast and ovarian cancer associated antigen gene SEQ ID 120.
XX
KW   Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW   nootropic; neurpprotective; antiviral; antiallergic; hepatotropic;
KW   antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
KW   antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW   Addison's disease; allergy; autoimmune haemolytic anaemia;
KW   autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW   multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW   cardiovascular disorder; wound healing; neurological disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200055173-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US005881.
XX
PR   12-MAR-1999;   99US-0124270P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-611515/58.
DR   P-PSDB; AAB58830.
XX
PT   New human breast and ovarian cancer associated gene sequences and the
PT   polypeptides encoded by these genes, useful in the prevention, treatment
PT   and diagnosis of cancer, immune disorders, cardiovascular disorders and
PT   neurological diseases.
XX
PS   Claim 1; Page 571; 1299pp; English.
XX
CC   Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC   proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC   associated with breast and ovarian cancer. Included in the invention are
CC   sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC   isolation and characterisation of the DNA and protein sequences of the
CC   invention. The breast and ovarian cancer associated DNA, protein, agonist
CC   or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic;
CC   neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
CC   antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;
CC   antifungal; antiparasitic and cardiant activity. The polynucleotide and
CC   protein sequences are used in the diagnosis of cancer, particularly
CC   breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
CC   and agonists may also be used in the diagnosis, prevention and treatment
CC   of immune disorders e.g. Addison's disease, allergies, autoimmune
CC   haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC   disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC   cardiovascular disorders such as myocardial ischaemias; wound healing;
CC   neurological diseases such as cerebral anoxia and epilepsy; and
CC   infectious diseases
XX
SQ   Sequence 1308 BP; 280 A; 325 C; 433 G; 269 T; 0 U; 1 Other;

  Query Match             98.0%;  Score 1255.8;  DB 3;  Length 1308;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 1268;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          9 CGGGGCTGGACTGTTCTAAGTGAGTTCGGGTGGGGAGCTTCACGAGGGGAGGCTGCTCT 68
              || | | |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 CGCGTCCGGACTGTTCTAAGTGAGTTCGGGTGGGGAGCTTCACGAGGGGAGGCTGCTCT 68

Qy         69 GTGAAGGAACCGCCTTTCTCTCCGCGTGTCTCACCCTTTTCTCCCCATATCTGTTTGGAC 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GTGAAGGAACCGCCTTTCTCTCCGCGTGTCTCACCCTTTTCTCCCCATATCTGTTTGGAC 128

Qy        129 ATGAGCTGAGGGCACGGTCGCGGGCGGTCAGCCCTGTTCGCAGCTACGGCGAGGAGGGGC 188
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        129 ATGAGCTGAGGGCACGGTCGCGGGCGGTCAG-CCTGTTCGCAGCTACGGCGAGGAGGGGC 187

Qy        189 GCGATTGTTCCTTGTTGCCGCTCCGCTTAGTGGCCGCGTCCATTCCGCGCGGTGTCCCGA 248
              |||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 GCGATTGYTCCTTGTTGCCGCTCCGCTTAGTGGCCGCGTCCATTCCGCGCGGTGTCCCGA 247

Qy        249 TTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGGCC 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 TTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGGCC 307

Qy        309 CCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGAAG 368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 CCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGAAG 367

Qy        369 GACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCCGG 428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 GACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCCGG 427

Qy        429 CTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGACTC 488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 CTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGACTC 487

Qy        489 CTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGAGAGGAG 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 CTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGAGAGGAG 547

Qy        549 AAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGCCC 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 AAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGCCC 607

Qy        609 ATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAGGCCTAT 668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 ATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAGGCCTAT 667

Qy        669 GGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCAGCGGGGC 728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 GGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCAGCGGGGC 727

Qy        729 TGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGG 788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 TGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGG 787

Qy        789 GACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAG 848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 GACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAG 847

Qy        849 AACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGG 908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 AACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGG 907

Qy        909 CCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCG 968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 CCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCG 967

Qy        969 AGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGG 1028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 AGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGG 1027

Qy       1029 CAGGAAACCTCTGGAGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGG 1088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 CAGGAAACCTCTGGAGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGG 1087

Qy       1089 AGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATC 1148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 AGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATC 1147

Qy       1149 CCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCC 1208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1148 CCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCC 1207

Qy       1209 CTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCA 1268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 CTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCA 1267

Qy       1269 CAAAAAAAAAAAA 1281
              |||||||||||||
Db       1268 CAAAAAAAAAAAA 1280


RESULT 2
AAC02135
ID   AAC02135 standard; cDNA; 465 BP.
XX
AC   AAC02135;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 2133.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-00200610.
XX
PR   26-FEB-1999;   99US-0122487P.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
DR   P-PSDB; AAG02129.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
```

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S   Claim 1; SEQ ID NO 2133; 71pp + Sequence Listing; English.
X
C   The present sequence is one of a large number of 5' ESTs derived from
C   mRNAs encoding secreted proteins. An ORF has been identified within the
C   sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
C   derived from 30 different tissues. EST sequences usually correspond
C   mainly to the 3' untranslated region (UTR) of the mRNA because they are
C   often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
C   well suited for isolating cDNA sequences derived from the 5' ends of
C   mRNAs and even in those cases where longer cDNA sequences have been
C   obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
C   mRNAs with intact 5' ends and can therefore be used to obtain full length
C   cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
C   gene therapy and chromosome mapping procedures. They are used to obtain
C   upstream regulatory sequences and to design expression and secretion
C   vectors
X
Q   Sequence 465 BP; 92 A; 117 C; 160 G; 90 T; 0 U; 6 Other;

 Query Match             35.8%;  Score 459.2;  DB 3;  Length 465;
 Best Local Similarity   98.5%;  Pred. No. 6.2e-117;
 Matches  458;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

y        247 GATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGG 306
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          1 GATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGG 60

y        307 CCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGA 366
             ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
b         61 CCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGRCAAGAGGAAATCCGGGA 120

y        367 AGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCC 426
             ||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
b        121 AGGACTTCGTGACCSAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCC 180

y        427 GGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGAC 486
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        181 GGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGAC 240

y        487 TCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGAGAGG 546
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        241 TCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGAGAGG 300

y        547 AGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGC 606
             |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
b        301 AGAAACGCCAGGCTGNNNCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGC 360

y        607 CCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAGGCCT 666
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||
b        361 CCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGARGCCT 420

y        667 ATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGA 711
             |||||||||||||||||||||||||||||||||||||||||| ||
b        421 ATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCGGA 465

ESULT 3
CH36439
D   ACH36439 standard; cDNA; 475 BP.
X
C   ACH36439;
X
T   13-OCT-2003  (first entry)
X
E   Human endothelial cell cDNA #4572.
X
W   Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
W   genome mapping; biodiversity; genetic disorder.
X
S   Homo sapiens.
X
N   US2003073623-A1.
X
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PD   17-APR-2003.
XX
PF   30-JUL-2001; 2001US-00918995.
XX
PR   30-JUL-2001; 2001US-00918995.
XX
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
XX
PI   Drmanac RT,  Labat I,  Stache-Crain B,  Dickson MC,  Jones LW;
XX
DR   WPI; 2003-615964/58.
XX
PT   New polynucleotide sequences obtained from various cDNA libraries, useful
PT   as hybridization probes, as oligomers for PCR, for chromosome and gene
PT   mapping, in the recombinant production of protein, or in generating
PT   antisense DNA or RNA.
XX
PS   Claim 1; SEQ ID NO 23651; 44pp; English.
XX
CC   The invention relates to an isolated polynucleotide comprising any one of
CC   38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC   determined by the technique of SBH (sequencing by hybridisation). Also
CC   included is a purified polypeptide comprising a sequence corresponding to
CC   a reading frame of the novel polynucleotide. The nucleic acid sequences
CC   are useful in diagnostics as expressed sequence tags (EST) for
CC   identifying expressed genes or for physical mapping of the human genome,
CC   in forensics, in assessing biodiversities, or in identifying mutations
CC   responsible for genetic disorders and other traits. The nucleotide
CC   sequences are also useful as hybridisation probes, as oligomers for PCR,
CC   for chromosome and gene mapping, in the recombinant production of
CC   protein, or in generating antisense DNA or RNA. The purified polypeptide
CC   is useful for generating antibodies specific for it. The present sequence
CC   is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ   Sequence 475 BP; 107 A; 115 C; 150 G; 96 T; 0 U; 7 Other;

  Query Match             31.1%;  Score 398.6;  DB 8;  Length 475;
  Best Local Similarity   97.8%;  Pred. No. 4e-100;
  Matches  404;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy        869 CTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGG 928
              |||  |   ||   ||| ||||||||||||||||||||||||||||||||||||||||||
Db         34 CTCGCGGAATTCCGCACGAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGG 93

Qy        929 GCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGACAGGGG 988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 GCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGACAGGGG 153

Qy        989 GGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGGAGACCT 1048
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 GGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGGAGACCT 213

Qy       1049 CATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCAAAGGAG 1108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 CATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCAAAGGAG 273

Qy       1109 GGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCCCCTCAG 1168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 GGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCCCCTCAG 333

Qy       1169 CCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCC 1228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCC 393

Qy       1229 AGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACAAAAAAAAAAAA 1281
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 AGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACAAAAAAAAAAAA 446

RESULT 4
ACH29232
ID   ACH29232 standard; cDNA; 407 BP.
XX
AC   ACH29232;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Human adult spleen cDNA #251.
XX
KW   Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW   genome mapping; biodiversity; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   US2003073623-A1.
XX
PD   17-APR-2003.
XX
PF   30-JUL-2001; 2001US-00918995.
XX
PR   30-JUL-2001; 2001US-00918995.
XX
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
XX
PI   Drmanac RT,  Labat I,  Stache-Crain B,  Dickson MC,  Jones LW;
XX
DR   WPI; 2003-615964/58.
XX
PT   New polynucleotide sequences obtained from various cDNA libraries, useful
PT   as hybridization probes, as oligomers for PCR, for chromosome and gene
PT   mapping, in the recombinant production of protein, or in generating
PT   antisense DNA or RNA.
XX
PS   Claim 1; SEQ ID NO 16444; 44pp; English.
XX
CC   The invention relates to an isolated polynucleotide comprising any one of
CC   38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC   determined by the technique of SBH (sequencing by hybridisation). Also
CC   included is a purified polypeptide comprising a sequence corresponding to
CC   a reading frame of the novel polynucleotide. The nucleic acid sequences
CC   are useful in diagnostics as expressed sequence tags (EST) for
CC   identifying expressed genes or for physical mapping of the human genome,
CC   in forensics, in assessing biodiversities, or in identifying mutations
CC   responsible for genetic disorders and other traits. The nucleotide
CC   sequences are also useful as hybridisation probes, as oligomers for PCR,
CC   for chromosome and gene mapping, in the recombinant production of
CC   protein, or in generating antisense DNA or RNA. The purified polypeptide
CC   is useful for generating antibodies specific for it. The present sequence
CC   is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ   Sequence 407 BP; 70 A; 120 C; 139 G; 78 T; 0 U; 0 Other;

  Query Match             30.8%;  Score 394.2;  DB 8;  Length 407;
  Best Local Similarity   98.0%;  Pred. No. 6.2e-99;
  Matches  399;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy        129 ATGAGCTGAGGGCACGGTCGCGGGCGGTCAGCCCTGTTCGCAGCTACGGCGAGGAGGGGC 188
              | ||||||||||||||||||||||||| |||||||||||||  |||||||||||||||||
Db          1 ACGAGCTGAGGGCACGGTCGCGGGCGGCCAGCCCTGTTCGCTTCTACGGCGAGGAGGGGC 60

Qy        189 GCGATTGTTCCTTGTTGCCGCTCCGCTTAGTGGCCGCGTCCATTCCGCGCGGTGTCCCGA 248
              ||||||| |||||| ||||||||||||||||||||||||||||||||||||| |||||||
Db         61 GCGATTGCTCCTTGCTGCCGCTCCGCTTAGTGGCCGCGTCCATTCCGCGCGGCGTCCCGA 120

Qy        249 TTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGGCC 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGGCC 180

Qy        309 CCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGAAG 368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGAAG 240

Qy        369 GACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCCGG 428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCCGG 300

Qy        429 CTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGACTC 488
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        301 CTCTCTGGTCCACTCAAGGAACAGTATGCTCATGAGCATGGCTTGAACTTCCAGAGACTC 360

Qy        489 CTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCG 535
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCG 407

RESULT 5
AAT23873
ID   AAT23873 standard; cDNA to mRNA; 337 BP.
XX
AC   AAT23873;
XX
DT   16-AUG-1996  (first entry)
XX
DE   Human gene signature HUMGS05801.
XX
KW   Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW   human; cloning; mapping; non-biased library; diagnosis; detection;
KW   cell typing; abnormal cell function; ss.
XX
OS   Homo sapiens.
XX
PN   WO9514772-A1.
XX
PD   01-JUN-1995.
XX
PF   11-NOV-1994;   94WO-JP001916.
XX
PR   12-NOV-1993;   93JP-00355504.
XX
PA   (MATS/) MATSUBARA K.
PA   (OKUB/) OKUBO K.
XX
PI   Matsubara K,  Okubo K;
XX
DR   WPI; 1995-206931/27.
XX
PT   Single-stranded DNA for identifying gene signatures - isolated from 3'-
PT   directed human cDNA library that reflects relative abundance of corresp.
PT   mRNA in specific human tissues.
XX
PS   Claim 1; Page 1475; 2245pp; Japanese.
XX
CC   A single-stranded DNA (or its complementary strand or the corresp. double
CC   -stranded DNA) which comprises one of the 7837 "GS" sequences given in
CC   AAT19001-T26837 and which is able to hybridise to part of human genomic
CC   DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were
CC   obtained from 3'-directed cDNA libraries prepared from various human
CC   tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using
CC   poly(T) as the sole primer. Since the 3'- untranslated sequence is unique
CC   to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise
CC   with specific mRNAs. Each library is constructed so as to reflect
CC   accurately the relative abundance of different mRNAs in the particular
CC   tissue from which it was derived. The appearance frequency of a given GS
CC   in a cDNA library can be determined (esp. using primers and probes
CC   derived from the GS sequences) as a means of diagnosing abnormal cell
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C   function or for recognising different cell types
X
Q   Sequence 337 BP; 82 A; 76 C; 94 G; 72 T; 0 U; 13 Other;

 Query Match            22.8%;  Score 292.6;  DB 2;  Length 337;
 Best Local Similarity  92.9%;  Pred. No. 8.4e-71;
 Matches  301;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

y         958 GATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGAT 1017
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
b           1 GATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTAAGGGGGTTGGTGGAT 60

y        1018 ATTGGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTCTCCATGGGGAAGACAGCCATGC 1077
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          61 ATTGGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTCTCCATGGGGAAGACAGCCATGC 120

y        1078 TCTTCAGGAGGAGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAAC 1137
              |||||||||||||||||||||||||||| |||||||||||||||| ||||||||||||||
b         121 TCTTCAGGAGGAGACTCCAAGGGCAAAGNAGGGTGTCTTGGCTGTNCTTGAAGGCGAAAC 180

y        1138 CCTGCCATATCCCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGAT 1197
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
b         181 CCTGCCATATCCCCAGTGCCAGTCCCCTCAGNCTGTGGTGGCCTTGCATCCTGACTGGAT 240

y        1198 GTTCTCAGCCCCTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGTGGATACTAATAAAC 1257
              ||||||||||| |||||||||||||||||||||||||||||||| |||||||| || ||
b         241 GTTCTCAGCCCNTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTNTGGATACTTATTAAA 300

y        1258 CTCTTGGAGCACAAAAAAAAAAAA 1281
              |   |   |      ||| | |||
b         301 CCTNTTTGGAGNCNCAAATANAAA 324

ESULT 6
AL20639/c
D   AAL20639 standard; cDNA; 502 BP.
X
C   AAL20639;
X
T   07-DEC-2001  (first entry)
X
E   Human breast cancer expressed polynucleotide 13096.
X
W   Human; breast cancer; cell marker; cytostatic; ss.
X
S   Homo sapiens.
X
N   WO200151628-A2.
X
D   19-JUL-2001.
X
F   10-JAN-2001; 2001WO-US000798.
X
R   14-JAN-2000; 2000US-0176077P.
R   14-MAR-2000; 2000US-0189167P.
R   24-MAR-2000; 2000US-0192099P.
R   29-MAR-2000; 2000US-0193480P.
R   15-MAY-2000; 2000US-0205230P.
R   09-JUN-2000; 2000US-0211315P.
R   25-JUL-2000; 2000US-0220534P.
X
A   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
X
I   Lillie J,  Xu Y,  Wang Y,  Steinmann K;
X
R   WPI; 2001-451856/48.
X
T   New peptide useful as a marker for the diagnosis of breast cancer.
X
S   Claim 1; Page 2324; 3695pp; English.
X
C   The invention relates to human breast cancer expressed polynucleotides
C   (AAL07544-AAL26789) and methods of assessing whether a patient is
```

```
CC   afflicted with breast cancer by examining the correlation between the
CC   expression of certain markers and the cancerous state of breast cells.
CC   The polynucleotides and encoded polypeptides are potential markers for
CC   detecting, diagnosing, monitoring, characterising treating and
CC   potentially preventing breast cancer. The polynucleotides and encoded
CC   polypeptides are also useful for isolating compounds with cytostatic
CC   activity
XX
SQ   Sequence 502 BP; 131 A; 148 C; 134 G; 89 T; 0 U; 0 Other;

  Query Match             9.8%;  Score 125;  DB 4;  Length 502;
  Best Local Similarity  96.2%;  Pred. No. 2.9e-24;
  Matches  128;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        337 TGCTGTTCAGCGGCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCA 396
              |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        495 TGCTGTTCAGCGGCAAGAGGAAATCCGGAAAGGACTTCGTGACCGAGGCGCTGCAGAGCA 436

Qy        397 GACTTGGAGCTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATG 456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 GACTTGGAGCTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATG 376

Qy        457 CTCAGGAGCATGG 469
              ||||||    |||
Db        375 CTCAGGTAGGTGG 363


RESULT 7
ABL30119
ID   ABL30119 standard; DNA; 570 BP.
XX
AC   ABL30119;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 41830.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX
PR   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Claim 1; SEQ ID NO 41830; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
```

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XX
SQ   Sequence 570 BP; 127 A; 148 C; 184 G; 111 T; 0 U; 0 Other;

  Query Match              6.4%;  Score 82;  DB 4;  Length 570;
  Best Local Similarity   51.9%;  Pred. No. 2.6e-12;
  Matches  268;  Conservative    0;  Mismatches  230;  Indels   18;  Gaps    3;

Qy         337 TGCTGTTCAGCGGCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCA 396
               | ||  ||||||||||| | || | ||| ||||| | | |  |||||  ||||||| | |
Db          14 TACTCATCAGCGGCAAGCGAAAGTGCGGCAAGGATTACATATCCGAGAGGCTGCAGCGGA 73

Qy         397 GACTTGGAGCTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATG 456
               || | ||  |       |||    || | ||  |||| |  ||  | |||    | |  |
Db          74 GATTGGGCTCCCGGTCGTGTA---TCGTTCGAATCTCAGAGCCCATTAAGTCGGAATGGG 130

Qy         457 CTCAGGAGCATGGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCT 516
               |||   |||     ||| || |  |    ||||| |      |  |||||||||||   |
Db         131 CTCGCAAGCTGCAGTTGGACCTGGACGCTCTCCTCGGTGATGGACCCTACAAGGAGAAGT 190

Qy         517 TTCGGAAGGACATGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTT 576
                 |||   ||||||||    ||| | || |||   ||       |||   |||| ||| |
Db         191 ACCGGCGCGACATGATTGTGTGGAGCGACGAGGTGCGGGCCCAGGACTACGGCTACTTCT 250

Qy         577 GCAGGAAGATTGTGGAGG------------GCATCTCCCAGCCCATCTGGCTGGTGAGTG 624
               || |   |    ||||||            ||        ||||  |   ||||| || |
Db         251 GCCGCGTGGCCATGGAGGAGGCGCTGAGTCGCCAGCAGACGCCCTACATTCTGGTCAGCG 310

Qy         625 ACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAGGCCTATGGGGCCG---TGACGC 681
               |    ||| |   |   ||||||  |||||| |||||| | || ||| | |
Db         311 ATGTGCGGCGCAAGAACGACATCAGGTGGTTCCGGGAGACTTACGGGCCGGAACGAGTCA 370

Qy         682 AGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGC 741
                 ||  | ||  |   | |        | |  ||       ||||| |||   || ||
Db         371 TCACCTTGCGTCTAACATCCCGTCCAGAAACGCGGTCTGCACGGGGATGGACCTTTACCG 430

Qy         742 CAGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGG 801
               ||||  | ||||||| |   || || || |  |||||  |  | |  |||     |   |
Db         431 CAGGAATAGACGATGTTCCCTCCGAGTGCGATCTGGATGATCTGGCCGACGGCTTCGACG 490

Qy         802 TCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGG 837
               |  |   |  | | |  |  ||||    || |||||
Db         491 TGGTGTTGGCCAACGACGAGGAACTCGACCAGGAGG 526

RESULT 8
AAL11749/c
ID   AAL11749 standard; cDNA; 568 BP.
XX
AC   AAL11749;
XX
DT   07-DEC-2001  (first entry)
XX
DE   Human breast cancer expressed polynucleotide 4206.
XX
KW   Human; breast cancer; cell marker; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200151628-A2.
XX
PD   19-JUL-2001.
XX
PF   10-JAN-2001; 2001WO-US000798.
XX
PR   14-JAN-2000; 2000US-0176077P.
PR   14-MAR-2000; 2000US-0189167P.
PR   24-MAR-2000; 2000US-0192099P.
PR   29-MAR-2000; 2000US-0193480P.
PR   15-MAY-2000; 2000US-0205230P.
PR   09-JUN-2000; 2000US-0211315P.
PR   25-JUL-2000; 2000US-0220534P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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XX
PI   Lillie J,  Xu Y,  Wang Y,  Steinmann K;
XX
DR   WPI; 2001-451856/48.
XX
PT   New peptide useful as a marker for the diagnosis of breast cancer.
XX
PS   Claim 1; Page 767; 3695pp; English.
XX
CC   The invention relates to human breast cancer expressed polynucleotides
CC   (AAL07544-AAL26789) and methods of assessing whether a patient is
CC   afflicted with breast cancer by examining the correlation between the
CC   expression of certain markers and the cancerous state of breast cells.
CC   The polynucleotides and encoded polypeptides are potential markers for
CC   detecting, diagnosing, monitoring, characterising treating and
CC   potentially preventing breast cancer. The polynucleotides and encoded
CC   polypeptides are also useful for isolating compounds with cytostatic
CC   activity
XX
SQ   Sequence 568 BP; 142 A; 170 C; 152 G; 100 T; 0 U; 4 Other;

  Query Match              6.0%;  Score 76.4;  DB 4;  Length 568;
  Best Local Similarity   76.8%;  Pred. No. 9.2e-11;
  Matches  119;  Conservative    0;  Mismatches   32;  Indels    4;  Gaps    2;

Qy         319 GCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGAA--GGACTTCGT 376
               |||  ||| || |  |       |     ||||||||||||||||||||  |   |||||
Db         549 GCGGGCCGAGGGTACTTGCTTGTTCAGCGGGCAAGAGGAAATCCGGGAAAGGACTTTCGT 490

Qy         377 GACCGA--GGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCCGGCTCTCT 434
               ||||||  |       ||||||||||||||||||||||||||||||||||||||||||||
Db         489 GACCGAAGGCGNTGCAAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCCGGCTCTCT 430

Qy         435 GGTCCACTCAAGGAACAGTATGCTCAGGAGCATGG 469
               ||||||||||||||||||||||||||||    |||
Db         429 GGTCCACTCAAGGAACAGTATGCTCAGGTAGGTGG 395

RESULT 9
ABL30118/c
ID   ABL30118 standard; DNA; 2673 BP.
XX
AC   ABL30118;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 41827.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX
PR   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Claim 1; SEQ ID NO 41827; 21pp + Sequence Listing; English.
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XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 2673 BP; 610 A; 738 C; 638 G; 687 T; 0 U; 0 Other;

  Query Match             4.7%;  Score 60.8;  DB 4;  Length 2673;
  Best Local Similarity   50.0%;  Pred. No. 3.7e-06;
  Matches  217;  Conservative    0;  Mismatches  202;  Indels   15;  Gaps    2;

Qy       419 TGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTT 478
             | || | ||  |||| |  ||  | |||    | |  ||||   |||     ||| || |
Db      1478 TATCGTTCGAATCTCAGAGCCCATTAAGTCGGAATGGGCTCGCAAGCTGCAGTTGGACCT 1419

Qy       479 CCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTG 538
               |    ||||| |      |  |||||||||||   |  |||   ||||||||    ||
Db      1418 GGACGCTCTCCTCGGTGATGGACCCTACAAGGAGAAGTACCGGCGCGACATGATTGTGTG 1359

Qy       539 GGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGG---- 594
             | | || |||   ||       |||   |||| ||| ||| |   |    ||||||
Db      1358 GAGCGACGAGGTGCGGGCCCAGGACTACGGCTACTTCTGCCGCGTGGCCATGGAGGAGGC 1299

Qy       595 --------GCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACAT 646
                     ||        ||||  |   ||||| || ||    ||| |   |   |||||
Db      1298 GCTGAGTCGCCAGCAGACGCCCTACATTCTGGTCAGCGATGTGCGGCGCAAGAACGACAT 1239

Qy       647 CCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGA 706
             |  |||||| |||||| | || ||| | |        |    |     | || | |
Db      1238 CAGGTGGTTCCGGGAGACTTACGGGCCGGAACGAGTCATCACCTTGCGTCTAACATCCCG 1179

Qy       707 GC---AGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTC 763
              |   | |  ||       ||||| |||   || ||  ||||  | ||||||| |   ||
Db      1178 TCCAGAAACGCGGTCTGCACGGGGATGGACCTTTACCGCAGGAATAGACGATGTTCCCTC 1119

Qy       764 AGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGA 823
              || || |  |||||  |  | |  |||     |   ||  |   |  | | |  |  ||
Db      1118 CGAGTGCGATCTGGATGATCTGGCCGACGGCTTCGACGTGGTGTTGGCCAACGACGAGGA 1059

Qy       824 ACAGCGCCTGGAGG 837
             ||    || |||||
Db      1058 ACTCGACCAGGAGG 1045


RESULT 10
ABL30184/c
ID   ABL30184 standard; DNA; 3406 BP.
XX
AC   ABL30184;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 42025.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX
PR   23-MAR-2000; 2000US-0191637P.
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PR   11-JUL-2000; 2000US-00614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Claim 1; SEQ ID NO 42025; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 3406 BP; 965 A; 833 C; 729 G; 879 T; 0 U; 0 Other;

  Query Match             4.7%;  Score 60.8;  DB 4;  Length 3406;
  Best Local Similarity   50.0%;  Pred. No. 4.1e-06;
  Matches  217;  Conservative    0;  Mismatches  202;  Indels   15;  Gaps    2;

Qy       419 TGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTT 478
             | || | ||  |||| |  ||  | |||    | |  ||||   |||     ||| || |
Db      3209 TATCGTTCGAATCTCAGAGCCCATTAAGTCGGAATGGGCTCGCAAGCTGCAGTTGGACCT 3150

Qy       479 CCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTG 538
               |    ||||| |      |  |||||||||||   |  |||   ||||||||    ||
Db      3149 GGACGCTCTCCTCGGTGATGGACCCTACAAGGAGAAGTACCGGCGCGACATGATTGTGTG 3090

Qy       539 GGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGG---- 594
             | | || |||   ||       |||   |||| ||| ||| |   |    ||||||
Db      3089 GAGCGACGAGGTGCGGGCCCAGGACTACGGCTACTTCTGCCGCGTGGCCATGGAGGAGGC 3030

Qy       595 --------GCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACAT 646
                     ||        ||||  |   ||||| || ||    ||| |   |   |||||
Db      3029 GCTGAGTCGCCAGCAGACGCCCTACATTCTGGTCAGCGATGTGCGGCGCAAGAACGACAT 2970

Qy       647 CCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGA 706
             |  |||||| |||||| | || ||| | |        |    |     | || | |
Db      2969 CAGGTGGTTCCGGGAGACTTACGGGCCGGAACGAGTCATCACCTTGCGTCTAACATCCCG 2910

Qy       707 GC---AGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTC 763
              |   | |  ||       ||||| |||   || ||  ||||  | ||||||| |   ||
Db      2909 TCCAGAAACGCGGTCTGCACGGGGATGGACCTTTACCGCAGGAATAGACGATGTTCCCTC 2850

Qy       764 AGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGA 823
              || || |  |||||  |  | |  |||     |   ||  |   |  | | |  |  ||
Db      2849 CGAGTGCGATCTGGATGATCTGGCCGACGGCTTCGACGTGGTGTTGGCCAACGACGAGGA 2790

Qy       824 ACAGCGCCTGGAGG 837
             ||    || |||||
Db      2789 ACTCGACCAGGAGG 2776


RESULT 11
ABN35477
ID   ABN35477 standard; DNA; 60 BP.
XX
AC   ABN35477;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human spliced transcript detection oligonucleotide SEQ ID NO:8225.
```

```
XX
KW   Human; mouse; rat; splice transcript; detection; RNA transcript;
KW   splice variant; transcriptome; oligonucleotide library; ss.
XX
OS   Homo sapiens.
XX
PN   WO200210449-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-IB001903.
XX
PR   28-JUL-2000; 2000US-0221607P.
PR   02-MAY-2001; 2001US-0287724P.
XX
PA   (COMP-) COMPUGEN INC.
XX
PI   Shoshan A,  Wasserman A,  Mintz E,  Mintz L,  Faigler S;
XX
DR   WPI; 2002-257383/30.
XX
PT   New oligonucleotide libraries comprising oligonucleotides which
PT   selectively hybridize to mRNAs transcribed from a transcription unit of a
PT   genome, useful for detecting tissue-, pathology-, and developmental-
PT   specific genes.
XX
PS   Example 1; SEQ ID NO 8225; 47pp; English.
XX
CC   The present invention describes oligonucleotide libraries for detecting
CC   messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC   )transcriptome comprises messenger RNAs transcribed from multiple
CC   transcription units that populate a genome. The library comprises several
CC   oligonucleotides, each capable of hybridising selectively to a set of
CC   messenger RNAs transcribed from a given transcription unit of the genome,
CC   which encodes one or more messenger RNA splice variants. The
CC   oligonucleotide libraries are useful for detecting mRNAs from a
CC   biological sample, in expression profiling studies, in qualitatively or
CC   quantitatively characterising the corresponding transcriptome, and in
CC   detecting RNA transcripts and splice variants of human or animal
CC   transcriptomes. The libraries may also be used as specialised mini
CC   libraries to detect transcripts of a sub-transcriptome under a particular
CC   biological or pathological state, and so allowing the detection of tissue
CC   - and pathology-specific genes such as those genes only expressed in
CC   specific tissue under a specific pathological condition; to detect
CC   developmental specific genes; and to detect RNA transcripts and splice
CC   variants of a transcriptome of a patient suffering from a particular
CC   disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC   rats, humans and mice, which are used in the exemplification of the
CC   present invention. N.B. The sequence data for this patent did not form
CC   part of the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 60 BP; 13 A; 17 C; 15 G; 15 T; 0 U; 0 Other;

  Query Match             4.7%;  Score 60;  DB 6;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-06;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1194 GGATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGTGGATACTAAT 1253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGTGGATACTAAT 60


RESULT 12
ADA71938
ID   ADA71938 standard; DNA; 2000 BP.
XX
AC   ADA71938;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Rice gene, SEQ ID 5263.
XX
KW   Plant; bacterial infection; fungal infection; viral infection; rice;
KW   gene; ds.
XX
OS   Oryza sativa.
XX
PN   WO2003000898-A1.
XX
PD   03-JAN-2003.
XX
PF   22-JUN-2001; 2001WO-IB001105.
XX
PR   22-JUN-2001; 2001WO-IB001105.
XX
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI   Chang H,  Chen W,  Cooper B,  Glazebrook J,  Goff SA,  Hou Y;
PI   Katagiri F,  Quan S,  Tao Y,  Whitham S,  Xie Z,  Zhu T,  Zou G;
XX
DR   WPI; 2003-175290/17.
XX
PT   Identifying at least one gene involved in plant resistance or response to
PT   pathogenic infection for conferring resistance or tolerance to a plant to
PT   bacterial, fungal or viral infection by determining or detecting plant
PT   gene expression.
XX
PS   Claim 27; SEQ ID NO 5263; 899pp; English.
XX
CC   The present invention relates to a method (M1) for identifying genes
CC   involved in plant resistance or response to pathogenic infection. M1
CC   comprises identifying a gene whose expression is significantly altered in
CC   the incompatible interaction of plant gene expression relative to
CC   expression of the gene in an uninfected plant, in a mutant plant that
CC   does not express a gene associated with response to pathogenic infection,
CC   or in a corresponding incompatible or compatible interaction. (M1) is
CC   useful for conferring resistance to resistance or tolerance to a plant to
CC   bacterial, fungal or viral infection. The present sequence was used to
CC   illustrate the invention.
XX
SQ   Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

  Query Match             4.6%;  Score 59.4;  DB 7;  Length 2000;
  Best Local Similarity   9.1%;  Pred. No. 8.1e-06;
  Matches   66;  Conservative  325;  Mismatches  336;  Indels    0;  Gaps    0;

Qy        286 CGAGGCGTGGCGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCA 345
              ::| : |:::  ::   : : ::   :   ::|:::::    : :: :: :   : :
Db          1 SRACSAGWKSRCSSWRGRRRMYMAGMMSCARMGSSRMSRKMGSMSKYRKCSSCGKCKMTT 60

Qy        346 GCGGCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAG 405
              : :: : :|::|     ::   |: : :  :::: : :: :  | :|::  :: : |: :
Db         61 RRKSKWYSASSASGRTGSKWSSGSYSGKGMKKRYKRSKRWRGRGRRGMRRSRMRWMGRYR 120

Qy        406 CTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGC 465
                 : | : | :      ::  :::::|: : |  |:   ::  ::|:  :   :|| |
Db        121 RCARSGRMAGGSGRMMGGKSRMSYWMWCYARGCGSCKRKKSKGGSWGKTCRRGARGGSGW 180

Qy        466 ATGGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGG 525
                |  :::  : : ::   :   :  |:::|::: :  :  :   :   ::      :|
Db        181 SSGAKYKSGSMSKRMWMSSCGRSGCGRRSAYSRYYGTSRKYGTYKKMTYYSASRCMRAYM 240

Qy        526 ACATGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGA 585
                 ::: |:::|  :: ::: :  :: :: :::::|:::   ::: || ::::  :::
Db        241 TTSYSWACSSYTWCRSKRRSMMWKMMRKMRWSRSYGWYSWSYKMWMCTAYKKSYYSRWCY 300

Qy        586 TTGTGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACA 645
               :: ||::|  ::    ::: : : ::: :: :   | :: : | : : ::     :||
Db        301 MYRGGGWRGATRYWGRGYMSRMAMMYKKMYWYRGYKGMKRGWWAGRMMMRSMCRWSKACY 360

Qy        646 TCCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGG 705
              :: ::  : |  :: |::::   ::::     : :  ::::|::   : :: : ::  ::
Db        361 YMRWRMWRMTRRRRWAKKSSRTSRRKKRKWCMRKRKYKRMRGYSRMRSCKRARWMKRCRS 420

Qy        706 AGCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAG 765
```

```
               : :::|| | :   ::: |   ::: ::  : :: : :  ::::          :|  |
Db        421 GRAWKMGCRGCMTCRMKSYGMMRWKSWKRMASKYKWMSRMYRWRKKKCSRTTMWGKTRGG 480

Qy        766 AATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAAC 825
              ::   |:| ::::: :  :|:::::   ::: ::: ::      : | :::      :
Db        481 MMGTMGRCRYKKRSGMKRKCRRRRWGRMYRMRWKRYYMSARYTMRYCARKKYSYSAARKA 540

Qy        826 AGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCAC 885
              :     :|       :: :::: :  :  :: :   :  ::|:: ::|: ::  ::  |
Db        541 RCWYRGKGYYWAGMWMKRYKRMYMYKMMWWYKRKYSKCSWYCKMSYYASCMKSARKAGAK 600

Qy        886 TAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATG 945
                :: :: | : : : : : ::  ::::   :    || |:|::: ::  :| ::: : :
Db        601 MCKRSKMSAWSKSMRSSRKCRKCASKRSSAKRYAMMGGMTSGSRMSRWKSYTCYWRKWGS 660

Qy        946 GGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGG 1005
               ::   ::::::: |: : |:: : :::|  : :::::  : ::  |: |  | :|::
Db        661 MKSTCTWMYYMSKYTYAKYGSYWRYRYRAWCMYMWRWYYYRYRSYMTYMAWYTSSTRMAM 720

Qy       1006 GGGTTGG 1012
               | :::|
Db        721 TGMKYSG 727

RESULT 13
ADB51434/c
ID   ADB51434 standard; DNA; 467 BP.
XX
AC   ADB51434;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:1976.
XX
KW   toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW   toxicity marker; toxicity progression; drug screening;
KW   primary rat hepatocyte toxicity modelling; gene; ds.
XX
OS   Rattus norvegicus.
XX
PN   WO2003065993-A2.
XX
PD   14-AUG-2003.
XX
PF   04-FEB-2003; 2003WO-US003482.
XX
PR   04-FEB-2002; 2002US-0353171P.
PR   13-MAR-2002; 2002US-0363534P.
PR   08-APR-2002; 2002US-0370248P.
PR   10-APR-2002; 2002US-0371134P.
PR   10-APR-2002; 2002US-0371135P.
PR   10-APR-2002; 2002US-0371150P.
PR   11-APR-2002; 2002US-0371413P.
PR   19-APR-2002; 2002US-0373601P.
PR   19-APR-2002; 2002US-0373602P.
PR   22-APR-2002; 2002US-0374139P.
PR   08-MAY-2002; 2002US-0378370P.
PR   09-MAY-2002; 2002US-0378652P.
PR   09-MAY-2002; 2002US-0378653P.
PR   09-MAY-2002; 2002US-0378665P.
PR   09-JUL-2002; 2002US-0394230P.
PR   09-JUL-2002; 2002US-0394253P.
PR   04-SEP-2002; 2002US-0407688P.
PR   28-JAN-2003; 2003US-0442900P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Mendrick D,  Porter M,  Johnson K,  Higgs B,  Castle A,  Orr M;
PI   Elashoff M;
XX
DR   WPI; 2003-731472/69.
XX
PT   Determining if a compound induces a toxic effect on a tissue or cell, for
PT   identifying hepatotoxic compounds, comprises comparing a gene expression
PT   profile of a tissue or cell sample to a database of Tox mean and non-Tox
PT   mean values.
XX
PS   Claim 44; SEQ ID NO 1976; 874pp; English.
XX
CC   The present invention describes a method for determining whether a
CC   compound induces a toxic effect on a tissue or cell. The method comprises
CC   preparing a gene expression profile of a tissue or cell sample exposed to
CC   the compound, and comparing the gene expression profile to a database
CC   comprising data or information on the Tox mean and non-Tox mean value.
CC   The method is useful for predicting or identifying at least one toxic
CC   effect, particularly hepatotoxicity, of a test or unknown compound. The
CC   genes listed in the specification are useful as diagnostic or toxicity
CC   markers for the prediction or identification of the physiological state
CC   of tissue or cell sample that has been exposed to a compound, or to
CC   identify or predict the toxic effects of a compound or an agent. These
CC   may also be used as markers for monitoring toxicity progression or for
CC   drug screening. The present sequence represents a primary rat hepatocyte
CC   toxicity modelling related gene sequence from the present invention.
XX
SQ   Sequence 467 BP; 99 A; 138 C; 93 G; 137 T; 0 U; 0 Other;

  Query Match              4.4%;  Score 56.8;  DB 9;  Length 467;
  Best Local Similarity   54.9%;  Pred. No. 2.3e-05;
  Matches  112;  Conservative    0;  Mismatches   92;  Indels    0;  Gaps    0;

Qy        816 GGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGA 875
              |||| ||||||| |||||||||| ||||||||||||||  | |||||||| |   ||| |
Db        467 GGAGATGAACAGTGCCTGGAGGATCAGTTGGAGAACCTTCTGGAATTTATTCATGCCAAA 408

Qy        876 CTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACT 935
              ||| ||     ||| |  ||| |||||| | | |     ||   || |          ||
Db        407 CTTCAGCGCTGAGGCTTGAGGGGTGAGCAGAGACTGATGGACCGGGCGAACCCTGCTTCT 348

Qy        936 CTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTA 995
                   |  |||| |      ||   |   |   ||   |   ||| || |   || | ||
Db        347 ACCAGATGTGGGTGCCCAGTCCTGGCTGAGGTCAGAAAACAGACAAACGGTCTGGCTTTA 288

Qy        996 GATTCTGAGGGGGTTGGTGGATAT 1019
               | |   || ||  ||  |   ||
Db        287 AACTTCCAGAGGAATGAGGAGGAT 264

RESULT 14
ACA37843
ID   ACA37843 standard; DNA; 2100 BP.
XX
AC   ACA37843;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Prokaryotic essential gene #19500.
XX
KW   Antisense; ds; prokaryotic essential gene; cell proliferation;
KW   drug design; gene.
XX
OS   Mycobacterium avium.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
```

```
PI   Wang L,  Zamudio C,  Malone C,  Haselbeck R,  Ohlsen KL,  Zyskind JW;
PI   Wall D,  Trawick JD,  Carr GJ,  Yamamoto R,  Forsyth RA,  Xu HH;
XX
DR   WPI; 2003-029926/02.
DR   P-PSDB; ABU33973.
XX
PT   New antisense nucleic acids, useful for identifying proteins or screening
PT   for homologous nucleic acids required for cellular proliferation to
PT   isolate candidate molecules for rational drug discovery programs.
XX
PS   Claim 14; SEQ ID NO 25713; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
CC   antisense nucleic acid; (4) an antibody capable of specifically binding
CC   the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC   proliferation or the activity of a gene in an operon required for
CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC   prokaryotic essential genes. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 2100 BP; 364 A; 732 C; 719 G; 285 T; 0 U; 0 Other;

  Query Match              4.0%;  Score 51;  DB 7;  Length 2100;
  Best Local Similarity   52.5%;  Pred. No. 0.0018;
  Matches  134;  Conservative    0;  Mismatches  120;  Indels    1;  Gaps    1;

Qy        121 GTTTGGACATGAGCTGAGGGCACGGTCGCGGGCGGTCAGCCCTGTTCGCAGCTACGGCGA 180
              ||| |   | |||| | | | |  | | | || || | ||   |     |    | ||||
Db       1620 GTTCGCCAAGGAGCGGCGCGAAGAGGCCCTGGAGGCCGGCAAGGACGCGATGGCCCGCGA 1679

Qy        181 GGAGGGGCGCGATTGTTCCTTGTTGCCGCTCCGCTTAGTGGCCGCGTCCATTCCGCGCGG 240
              || | | ||||   |      ||||| || |    |    ||||  |||| |  ||||||
Db       1680 GGTGCGCCGCGGCGGACTTCCGTTGCAGCGCTTGGTCAATGCCGAATCCA-TGAGCGCGG 1738

Qy        241 TGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCC 300
              || ||||      |   || |  || ||||| ||      || |||||   |||  || |
Db       1739 TGGCCCGCGAACTGCACTACGCCGACGTGTCGGCCCTCTACACCGCGATCGGTGAGGGGC 1798

Qy        301 CCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAAT 360
                 || |  | | |   |  |  | ||||||| |      | || ||||||      |
Db       1799 ATGTGTCGGCCCGGCACGTGGTGCAGCGGCTGCTGGCCGAGCTCGGCGGCATCGACCAGG 1858

Qy        361 CCGGGAAGGACTTCG 375
              ||| | ||||| |||
Db       1859 CCGAGGAGGACCTCG 1873


RESULT 15
AAC93822/c
```

```
ID   AAC93822 standard; cDNA; 500 BP.
XX
AC   AAC93822;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:317.
XX
KW   Cat flea; hindgut and Malpighian tubule nucleic acid; HMT;
KW   flea infestation; vaccine; antiparasitic; therapeutic target; diagnosis;
KW   detection; ss.
XX
OS   Ctenocephalides felis.
XX
PN   WO200061621-A2.
XX
PD   19-OCT-2000.
XX
PF   07-APR-2000; 2000WO-US009437.
XX
PR   09-APR-1999;   99US-0128704P.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Brandt KS,  Gaines PJ,  Stinchcomb DT,  Wisnewski N;
XX
DR   WPI; 2000-656323/63.
XX
PT   Flea Malpighian tubule and head and nerve cord tissue derived nucleic
PT   acids useful for the prevention, diagnosis and treatment of flea
PT   infestations.
XX
PS   Claim 26; Page 350; 964pp; English.
XX
CC   The invention relates to novel cat flea (Ctenocephalides felis) nucleic
CC   acids which are expressed in hindgut and Malpighian tubule (HMT) tissue
CC   or head and nerve cord (HNC) tissue. The invention also relates to the
CC   encoded proteins. The invention additionally encompasses expression
CC   constructs, recombinant viruses and recombinant cells comprising the
CC   nucleic acids of the invention, recombinant production of the proteins,
CC   antibodies against the proteins, a method of identifying inhibitors of
CC   the proteins, and compositions comprising the inhibitors for
CC   administration to an animal. The nucleic acids, and the proteins they
CC   encode may be used in the prevention, treatment and diagnosis of diseases
CC   associated with flea infestations. For example, the nucleic acids may be
CC   used to produce an HMT or HNC protein according to standard recombinant
CC   DNA methodology by inserting the nucleic acids into a host cell and
CC   culturing the cell to express the protein. The HMT and HNC nucleic acids
CC   may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect
CC   and quantitate the presence of cat flea or other homologous nucleic acid
CC   sequences in samples. They may also be used to study the expression and
CC   function of the proteins and their role in metabolism. The HMT and HNC
CC   proteins may be used as antigens in the production of specific
CC   antibodies, and in assays to identify modulators (agonists and
CC   antagonists) of HMT and/or HNC protein expression and activity. The anti-
CC   HMT/HNC protein antibodies and antagonists may also be used to
CC   downregulate protein expression and activity. The antibodies may also be
CC   used as diagnostic agents for detecting the presence of flea polypeptides
CC   in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The
CC   present sequence represents a cat flea HMT cDNA of the invention
XX
SQ   Sequence 500 BP; 157 A; 81 C; 43 G; 200 T; 0 U; 19 Other;

  Query Match              3.8%;  Score 48.8;  DB 3;  Length 500;
  Best Local Similarity   48.4%;  Pred. No. 0.0039;
  Matches  119;  Conservative    1;  Mismatches  126;  Indels    0;  Gaps    0;

Qy        566 AGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGA 625
              | | || ||||     | |  |    | |  || ||  | || || ||  | || |||||
Db        441 ATGGTTATTTTTGTAAAGGGCTTGCCAAGCAATTTCAAAACCTATTTGCATAGTTAGTGA 382

Qy        626 CACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGAC 685
               |  || ||     | || || ||  | ||||||   ||    ||||| ||          ||
Db        381 TATCCGCAGGAACNCAGATATAAAATGGTTTATTGAAAAATATGGTGCTAAAGTTATAAC 322

Qy        686 GGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGG 745
                |  |  ||          |    |  ||| |    || || |||   || ||   |||
Db        321 NATTAGAATTAATTGCAGTAAATGCATTCGANAATNTCGAGGTTGGAAATTTACNGAAGG 262

Qy        746 GGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCAT 805
               || || |||| ||  |  |||||||   |  | || |  |   |||  || |  |:  |
Db        261 TGTTGATGATGTTGCNTNTGAATGTGATTTANATAATTATGAAAACTGGGATTTTGKTCT 202

Qy        806 CGAGAA 811
               |  ||
Db        201 TGTTAA 196

Search completed: March 10, 2004, 10:59:01
Job time : 315.77 secs
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                 GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:          March 10, 2004, 08:38:17 ; Search time 3263.87 Seconds
                                             (without alignments)
                                             17011.249 Million cell updates/sec

Title:           US-10-084-817-1
Perfect score:   1281
Sequence:        1 gttctgggcggggctggact.........tggagcacaaaaaaaaaaaa 1281

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters:      6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        GenEmbl:*
                 1:  gb_ba:*
                 2:  gb_htg:*
                 3:  gb_in:*
                 4:  gb_om:*
                 5:  gb_ov:*
                 6:  gb_pat:*
                 7:  gb_ph:*
                 8:  gb_pl:*
                 9:  gb_pr:*
                 10:  gb_ro:*
                 11:  gb_sts:*
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                 13:  gb_un:*
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                 20:  em_om:*
                 21:  em_or:*
                 22:  em_ov:*
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                 25:  em_pl:*
                 26:  em_ro:*
                 27:  em_sts:*
                 28:  em_un:*
                 29:  em_vi:*
                 30:  em_htg_hum:*
                 31:  em_htg_inv:*
                 32:  em_htg_other:*
                 33:  em_htg_mus:*
                 34:  em_htg_pln:*
                 35:  em_htg_rod:*
                 36:  em_htg_mam:*
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                 39:  em_htgo_hum:*
                 40:  em_htgo_mus:*
                 41:  em_htgo_other:*

      Pred. No. is the number of results predicted by chance to have a
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      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                        SUMMARIES
                     %
Result             Query
  No.     Score    Match Length DB  ID                            Description
-------------------------------------------------------------------------------
      1  1271.4    99.3   1339  9  BC006089                       BC006089 Homo sapi
      2    1215    94.8   1225  9  BC007694                       BC007694 Homo sapi
      3     984    76.8   1002  9  HUMPHKI                        L77213 Homo sapien
      4   927.6    72.4   1178  9  AK130234                       AK130234 Homo sapi
      5   577.4    45.1    579  12  AY335584                       AY335584 Synthetic
      6     528    41.2   8862  9  AF026069                       AF026069 Homo sapi
      7     528    41.2 110000  2  AL672265_1                     Continuation (2 of
      8     528    41.2 175826  2  AC021890                       AC021890 Homo sapi
c     9     528    41.2 182166  9  AL451085                       AL451085 Human DNA
c    10     528    41.2 195189  2  AC034149                       AC034149 Homo sapi
     11   459.2    35.8    465  6  AX886270                       AX886270 Sequence
     12   459.2    35.8    465  6  BD025880                       BD025880 Sequence
     13   359.6    28.1   1008  10  BC028659                       BC028659 Mus muscu
c    14   333.6    26.0    422  11  G22398                         G22398 human STS W
     15   317.2    24.8    419  6  AR415566                       AR415566 Sequence
     16   317.2    24.8    419  6  BD111119                       BD111119 EST and e
     17   270.8    21.1    317  4  PIGPHKI                        L77214 Sus scrofa
c    18   154.8    12.1 110000  2  AL672265_2                     Continuation (3 of
c    19   154.8    12.1 110000  2  AL672265_3                     Continuation (4 of
     20     139    10.9 180590  2  AC121079                       AC121079 Mus muscu
c    21     139    10.9 197096  10  AC104329                       AC104329 Mus muscu
     22     127     9.9 219649  2  AC133222                       AC133222 Rattus no
c    23     127     9.9 228051  2  AC097434                       AC097434 Rattus no
     24      82     6.4   1176  3  AY119197                       AY119197 Drosophil
c    25    71.4     5.6    501  6  AX824946                       AX824946 Sequence
     26    62.2     4.9 171330  5  AL929040                       AL929040 Zebrafish
c    27    62.2     4.9 176379  5  AL845419                       AL845419 Zebrafish
c    28    60.8     4.7  54115  2  AC018149                       AC018149 Drosophil
     29    60.8     4.7  60040  3  AC005128                       AC005128 Drosophil
c    30    60.8     4.7 155557  3  AC099020                       AC099020 Drosophil
c    31    60.8     4.7 290667  3  AE003663                       AE003663 Drosophil
c    32    59.6     4.7 125020  9  AF429315                       AF429315 Homo sapi
     33    59.4     4.6   2000  6  AX655393                       AX655393 Sequence
     34    58.6     4.6 125020  9  AF429315                       AF429315 Homo sapi
c    35    53.8     4.2  37909  9  AC002105                       AC002105 Genomic s
c    36      49     3.8   7218  6  I66494                         I66494 Sequence 14
     37      48     3.7   2260  8  AK121306                       AK121306 Oryza sat
     38      48     3.7 179021  8  OSJN00140                      AL662937 Oryza sat
     39    47.4     3.7 118504  9  AC094080                       AC094080 Homo sapi
     40    47.4     3.7 170797  9  AC011379                       AC011379 Homo sapi
     41    47.4     3.7 210675  2  AC026272                       AC026272 Homo sapi
c    42    46.4     3.6  67480  7  AY129334                       AY129334 Mycobacte
c    43    45.8     3.6 152838  2  AC011589                       AC011589 Homo sapi
c    44    44.4     3.5 247017  2  AC105601                       AC105601 Rattus no
     45    43.8     3.4  45519  1  FVBPOAD2A                      D26094 Flavobacter

                                        ALIGNMENTS

RESULT 1
BC006089
LOCUS       BC006089                1339 bp    mRNA    linear   PRI 12-NOV-2003
DEFINITION  Homo sapiens phosphomevalonate kinase, mRNA (cDNA clone MGC:12661
            IMAGE:3604167), complete cds.
ACCESSION   BC006089
VERSION     BC006089.1  GI:13543886
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1339)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1339)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-APR-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
            Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
            Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
            Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
            Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
            Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
            Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
            George Yang, Scott Zuyderduyn, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 18 Row: f Column: 9
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 20127505.
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                     Phosphomevalonate kinase (EC:2.7.4.2) catalyses the
                     phosphorylation of 5-phosphomevalonate into
                     5-diphosphomevalonate, an essential step in isoprenoid
                     biosynthesis via the mevalonate pathway. This family
                     represents the animal type of the enzyme. The other is the
                     ERG8 type, found in plants and fungi, and some bacteria
                     (see pfam00288)"
                     /db_xref="CDD:pfam04275"
ORIGIN

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  Matches 1275;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 GTTCTGGGCGGGGCTGGACTGTTCTAAGTGAGTTCGGGTGGGGGAGCTTCACGAGGGGAG 60
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Qy        481 AGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGG 540
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RESULT 2
BC007694
LOCUS       BC007694                1225 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens phosphomevalonate kinase, mRNA (cDNA clone MGC:11362
            IMAGE:3954909), complete cds.
ACCESSION   BC007694
VERSION     BC007694.2  GI:33871285
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1225)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
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            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1225)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-MAY-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     On Aug 19, 2003 this sequence version replaced gi:14043402.
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 15 Row: k Column: 14.
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                     Phosphomevalonate kinase (EC:2.7.4.2) catalyzes the
                     phosphorylation of 5-phosphomevalonate into
                     5-diphosphomevalonate, an essential step in isoprenoid
                     biosynthesis via the mevalonate pathway. This family
                     represents the animal type of the enzyme. The other is the
                     ERG8 type, found in plants and fungi, and some bacteria
                     (see pfam00288)"
                     /db_xref="CDD:pfam04275"
ORIGIN

  Query Match             94.8%;  Score 1215;  DB 9;  Length 1225;
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  Matches 1215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           67 CTGTGAAGGAACCGCCTTTCTCTCCGCGTGTCTCACCCTTTTCTCCCCATATCTGTTTGG 126
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Qy        1267 CACAAAAAAAAAAAA 1281
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Db        1201 CACAAAAAAAAAAAA 1215


RESULT 3
HUMPHKI
LOCUS       HUMPHKI                 1002 bp    mRNA    linear   PRI 24-JUL-1996
DEFINITION  Homo sapiens phosphomevalonate kinase mRNA, complete cds.
ACCESSION   L77213
VERSION     L77213.1  GI:1294781
KEYWORDS    cholesterol biosynthesis; kinase; peroxisomal; phosphomevalonate
            kinase.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1002)
  AUTHORS   Chambliss,K.L., Slaughter,C.A., Schreiner,R., Hoffmann,G.F. and
            Gibson,K.M.
  TITLE     Molecular cloning of human phosphomevalonate kinase and
            identification of a consensus peroxisomal targeting sequence
  JOURNAL   J. Biol. Chem. 271 (29), 17330-17334 (1996)
  MEDLINE   96291886
   PUBMED   8663599
COMMENT     Original source text: Homo sapiens (clone library: Stratagene)
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                     /note="(vector lambda ZAPII)"
     mRNA            1. .1002
     5'UTR           1. .35
     CDS             36. .614
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                     /evidence=experimental
                     /product="phosphomevalonate kinase"
                     /protein_id="AAC37593.1"
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                     /translation="MAPLGGAPRLVLLFSGKRKSGKDFVTEALQSRLGADVCAVLRLS
                     GPLKEQYAQEHGLNFQRLLDTSTYKEAFRKDMIRWGEEKRQADPGFFCRKIVEGISQP
                     IWLVSDTRRVSDIQWFREAYGAVTQTVRVVALEQSRQQRGWVFTPGVDDAESECGLDN
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     misc_feature    603. .611
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     3'UTR           615. .1002
     polyA_signal    984. .989
     polyA_site      1002
ORIGIN

  Query Match             76.8%;  Score 984;  DB 9;  Length 1002;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-233;
  Matches  984;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         286 CGAGGCGTGGCGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCA 345
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          19 CGAGGCGTGGCGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCA 78

Qy         346 GCGGCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAG 405
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          79 GCGGCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAG 138

Qy         406 CTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGC 465
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Db        139 CTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGC 198

Qy        466 ATGGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGG 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 ATGGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGG 258

Qy        526 ACATGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGA 585
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Qy        586 TTGTGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACA 645
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Db        319 TTGTGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACA 378

Qy        646 TCCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGG 705
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Db        379 TCCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGG 438

Qy        706 AGCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAG 765
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Db        439 AGCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAG 498

Qy        766 AATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAAC 825
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 AATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAAC 558

Qy        826 AGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCAC 885
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Db        559 AGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCAC 618

Qy        886 TAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATG 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 TAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATG 678

Qy        946 GGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGG 1005
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Db        679 GGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGG 738

Qy       1006 GGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTCTCCATGGGGA 1065
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Db        739 GGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTCTCCATGGGGA 798

Qy       1066 AGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTGCT 1125
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Db        799 AGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTGCT 858

Qy       1126 TGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCA 1185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 TGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCA 918

Qy       1186 TCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGTGG 1245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 TCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGTGG 978

Qy       1246 ATACTAATAAACCTCTTGGAGCAC 1269
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Db        979 ATACTAATAAACCTCTTGGAGCAC 1002


RESULT 4
AK130234
LOCUS       AK130234                1178 bp    mRNA    linear   PRI 10-SEP-2003
DEFINITION  Homo sapiens cDNA FLJ26724 fis, clone PNC05489.
ACCESSION   AK130234
VERSION     AK130234.1  GI:34526995
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Suzuki,O., Sasaki,N., Aotsuka,S., Shoji,T., Ichihara,T.,
            Shiohata,N., Matsumoto,K., Hirano,M., Sano,S., Nomura,R.,
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            Yoshikawa,Y., Matsumura,Y., Moriya,S., Chiba,E., Momiyama,H.,
            Onogawa,S., Kaeriyama,S., Satoh,N., Matsunawa,H., Takahashi,E.,
            Kataoka,R., Kuga,N., Kuroda,A., Satoh,I., Kamata,K., Takami,S.,
            Terashima,Y., Watanabe,M., Suzuki,Y., Hata,H., Nakagawa,K.,
            Mizuno,S., Morinaga,M., Kawamura,M., Sugiyama,T., Irie,R.,
            Otsuki,T., Sato,H., Nishikawa,T., Sugiyama,A., Kawakami,B.,
            Nagai,K., Isogai,T. and Sugano,S.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1178)
  AUTHORS   Sugano,S. and Suzuki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science,
            University of Tokyo, Laboratory of Genome Structure, Human Genome
            Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
            (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
            Fax:81-3-5449-5416)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction and 5'-end one pass sequencing: Institute of Medical
            Science, University of Tokyo, Laboratory of Genome Structure, Human
            Genome Center; 3'-end one pass sequencing: RAB; clone selection for
            full insert sequencing: RAB and Helix Research Institute.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="PNC05489"
                     /tissue_type="pancreas"
                     /clone_lib="PNC"
                     /note="cloning vector: pME18SFL3"
ORIGIN

  Query Match             72.4%;  Score 927.6;  DB 9;  Length 1178;
  Best Local Similarity   86.5%;  Pred. No. 2.6e-219;
  Matches 1113;  Conservative    0;  Mismatches   19;  Indels  154;  Gaps    2;

Qy         30 GAGTTCGGGTGGGGAGCTTCACGAGGGGAGGCTGCTCTGTGAAGGAACCGCCTTTCTCT 89
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Db          1 GAGTTCGGGTGGGGAGCTTCACGAGGGGAGGCTGCTCTGTGAAGGAACCGCCTTTCTCT 60

Qy         90 CCGCGTGTCTCACCCTTTTCTCCCCATATCTGTTTGGACATGAGCTGAGGGCACGGTCGC 149
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Db         61 CCGCGTGTCTCACCCTTTTCTCCCCATATCTGTTTGGACATGAGCTGAGGGCACGGTCGC 120

Qy        150 GGGCGGTCAGCCCTGTTCGCAGCTACGGCGAGGAGGGGCGCGATTGTTCCTTGTTGCCGC 209
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Db        121 GGGCGGTCAGCCCTGTTCGCAGCTACGGCGAGGAGGGGCGCGATTGCTCCTTGTTGCCGC 180

Qy        210 TCCGCTTAGTGGCCGCGTCCATTCCGCGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTG 269
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Db        181 TCCGCTTAGTGGCCGCGTCCATTCCGCGCGGTGTCCCGATTTTAG---------------- 225

Qy        270 TCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGG 329

Db        226 ------------------------------------------------------------ 225

Qy        330 CTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTG 389
                                               |||||||||||||||||||||||||||
Db        226 ---------------------------------GGGAAGGACTTCGTGACCGAGGCGCTG 252

Qy        390 CAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAA 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 CAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAA 312

Qy        450 CAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAG 509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 CAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAG 372

Qy        510 GAGGCCTTTCGGAAGGACATGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGC 569
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Db          373 GAGGCCTTTCGGAAGGACATGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGC 432

Qy          570 TTCTTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACA 629
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Db          433 TTCTTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACA 492

Qy          630 CGGAGAGTGTCTGACATCCAGTGGTTTCGGGAG--------------------------- 662
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Db          493 CGGAGAGTGTCTGACATCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTT 552

Qy          663 -------------------GCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTT 703
                                   |   | |    ||||||||||||||||||||||||||||||
Db          553 CAGCGGCAAGAGGAAATCCGGGAAGGACTTCGTGACGCAGACGGTCCGCGTTGTAGCGTT 612

Qy          704 GGAGCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTC 763
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Db          613 GGAGCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTC 672

Qy          764 AGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGA 823
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          673 AGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGA 732

Qy          824 ACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTC 883
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Db          733 ACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTC 792

Qy          884 ACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAA 943
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Db          793 ACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAA 852

Qy          944 TGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGA 1003
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          853 TGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGA 912

Qy         1004 GGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTCTCCATGGG 1063
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Db          913 GGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTCTCCATGGG 972

Qy         1064 GAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTG 1123
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Db          973 GAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTG 1032

Qy         1124 CTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTG 1183
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1033 CTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTG 1092

Qy         1184 CATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGT 1243
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Db         1093 CATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGT 1152

Qy         1244 GGATACTAATAAACCTCTTGGAGCAC 1269
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Db         1153 GGATACTAATAAACCTCTTGGAGCAC 1178


RESULT 5
AY335584
LOCUS       AY335584                 579 bp    mRNA    linear   SYN 15-OCT-2003
DEFINITION  Synthetic construct Homo sapiens phosphomevalonate kinase (PMVK)
            mRNA, partial cds.
ACCESSION   AY335584
VERSION     AY335584.1  GI:33303794
KEYWORDS    FLI_CDNA.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 579)
  AUTHORS   Park,J., Rolfs,A., Hu,Y., Shen,B., Vannberg,F., Moreira,D.,
            Kelley,T., Zuo,D., Raphael,J., Baqui,M., Jepson,D., Harlow,E.,
            LaBaer,J. and Brizuela,L.
  TITLE     Cloning of human full-length CDS FLEXGene kinases in
            recombinational vector system
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 579)
  AUTHORS   Park,J., Rolfs,A., Hu,Y., Shen,B., Vannberg,F., Moreira,D.,
            Kelley,T., Zuo,D., Raphael,J., Baqui,M., Jepson,D., Harlow,E.,
            LaBaer,J. and Brizuela,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUL-2003) Biological Chemistry and Molecular
            Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
            Cambridge, MA 02141-2023, USA
COMMENT     This CDS clone is a part of a collection of human full-length
            expression clones generated by Harvard Institute of Proteomics.
            Each CDS has been cloned without stop-codon (to allow fusion with
            C-terminal tag). The CDS has been directionally cloned using BD
            In-Fusion(TM) cloning system between the SalI and HindIII sites of
            the pDNR-Dual vector. Additional sequences in the clone:  'ACC'
            after SalI site and before 'ATG' to provide Kozak consensus
            sequence; 'GG' after last codon and before HindIII site to maintain
            reading frame.
FEATURES             Location/Qualifiers
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                     /clone_lib="MGC clone templates"
                     /lab_host="DH5alpha T1 resistant"
                     /note="Vector: pDNR-Dual"
     gene            1. .>579
                     /gene="PMVK"
     CDS             1. .>579
                     /gene="PMVK"
                     /note="Mutations: Stop->Leu"
                     /codon_start=1
                     /transl_table=11
                     /product="phosphomevalonate kinase"
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                     /db_xref="GI:33303795"
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                     GPLKEQYAQEHGLNFQRLLDTSTYKEAFRKDMIRWGEEKRQADPGFFCRKIVEGISQP
                     IWLVSDTRRVSDIQWFREAYGAVTQTVRVVALEQSRQQRGWVFTPGVDDAESECGLDN
                     FGDFDWVIENHGVEQRLEEQLENLIEFIRSRLL"
ORIGIN

  Query Match            45.1%;  Score 577.4;  DB 12;  Length 579;
  Best Local Similarity  99.8%;  Pred. No. 2.3e-132;
  Matches  578;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          303 ATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCC 362
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Db            1 ATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCC 60

Qy          363 GGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTC 422
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           61 GGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTC 120

Qy          423 CTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAG 482
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 CTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAG 180

Qy          483 AGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGA 542
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 AGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGA 240

Qy          543 GAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCC 602
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 GAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCC 300

Qy          603 CAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAG 662
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 CAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAG 360

Qy          663 GCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCAG 722
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Db          361 GCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCAG 420
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Qy        723 CGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAAC 782
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Db        421 CGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAAC 480

Qy        783 TTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAG 842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAG 540

Qy        843 TTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAG 881
              ||||||||||||||||||||||||||||||||||||| |
Db        541 TTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTTG 579


RESULT 6
AF026069
LOCUS       AF026069                8862 bp    DNA     linear   PRI 12-MAY-1999
DEFINITION  Homo sapiens phosphomevalonate kinase (HUMPMKI) gene, partial cds.
ACCESSION   AF026069
VERSION     AF026069.1  GI:3647227
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8862)
  AUTHORS   Olivier,L.M., Chambliss,K.L., Gibson,K.M. and Krisans,S.K.
  TITLE     Characterization of phosphomevalonate kinase: chromosomal
            localization, regulation, and subcellular targeting
  JOURNAL   J. Lipid Res. 40 (4), 672-679 (1999)
  MEDLINE   99208737
   PUBMED   10191291
REFERENCE   2  (bases 1 to 8862)
  AUTHORS   Chambliss,K.L. and Gibson,K.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-SEP-1997) Institute of Metabolic Disease, Baylor
            University Medical Center, 3812 Elm St., Dallas, TX 75226, USA
REFERENCE   3  (bases 1 to 8862)
  AUTHORS   Chambliss,K.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Pediatrics, University of Texas
            Southwestern Medical Center, 5323 Harry Hines Blvd., Dallas, TX
            75235-9063, USA
  REMARK    Sequence update by submitter
COMMENT     On Sep 25, 1998 this sequence version replaced gi:3445541.
FEATURES             Location/Qualifiers
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                     /product="phosphomevalonate kinase"
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                     /codon_start=2
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                     "
ORIGIN

  Query Match             41.2%;  Score 528;  DB 9;  Length 8862;
  Best Local Similarity   100.0%;  Pred. No. 4e-120;
  Matches  528;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        743 AGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGT 802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7715 AGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGT 7774

Qy        803 CATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATT 862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7775 CATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATT 7834

Qy        863 TATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGG 922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7835 TATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGG 7894

Qy        923 GGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGA 982
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Db       7895 GGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGA 7954

Qy        983 CAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGG 1042
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Db       7955 CAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGG 8014

Qy       1043 AGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCA 1102
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Db       8015 AGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCA 8074

Qy       1103 AAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCC 1162
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Db       8075 AAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCC 8134

Qy       1163 CCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAA 1222
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Db       8135 CCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAA 8194

Qy       1223 GAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACA 1270
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db       8195 GAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACA 8242


RESULT 7
AL672265_1
WPCOMMENT
  Sequence split into 6 fragments  LOCUS AL672265 Accession AL672265
     Fragment Name       Begin      End
     AL672265_0              1      110000
     AL672265_1         100001      210000
     AL672265_2         200001      310000
     AL672265_3         300001      410000
     AL672265_4         400001      510000
     AL672265_5         500001      534015
Continuation (2 of 6) of AL672265 from base 100001 (AL672265 Homo sapiens chromosome 1 

  Query Match             41.2%;  Score 528;  DB 2;  Length 110000;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-120;
  Matches  528;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        743 AGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGT 802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      65400 AGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGT 65459

Qy        803 CATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATT 862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      65460 CATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATT 65519

Qy        863 TATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGG 922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      65520 TATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGG 65579

Qy        923 GGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGA 982
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      65580 GGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGA 65639

Qy        983 CAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGG 1042
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Db      65640 CAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGG 65699

Qy       1043 AGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCA 1102
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Db      65700 AGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCA 65759

Qy       1103 AAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCC 1162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      65760 AAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCC 65819

Qy       1163 CCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAA 1222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      65820 CCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAA 65879

Qy       1223 GAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACA 1270
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Db      65880 GAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACA 65927


RESULT 8
AC021890
LOCUS       AC021890               175826 bp    DNA     linear   HTG 10-NOV-2000
DEFINITION  Homo sapiens chromosome 3 clone RP11-498A2, WORKING DRAFT SEQUENCE,
            22 unordered pieces.
ACCESSION   AC021890
VERSION     AC021890.12  GI:11128300
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 175826)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
            Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
            Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
            Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
            Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
            Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
            Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
            Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
            Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
            Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
            Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
            Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
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            Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
            Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
            Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
            Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N.,
            Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
            Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
            Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
            Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
            Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
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            Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
            Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
            Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.
            and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 175826)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JAN-2000) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Nov 9, 2000 this sequence version replaced gi:9719697.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: HMZE
                Center clone name: RP11-498A2
            -------------- Summary Statistics
                Sequencing vector: M13; L08821
                Chemistry: Dye-terminator Big Dye: 100% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 144734 bases at least Q40
                Consensus quality: 162873 bases at least Q30
                Consensus quality: 169424 bases at least Q20
                Estimated insert size: 170770; sum-of-contigs estimation
                Quality coverage: 0x in Q20 bases; agarose-fp estimation
                Quality coverage: 3.3x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *    (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 22 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    21031: contig of 21031 bp in length
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            *    21132    40475: contig of 19344 bp in length
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            *    40576    57617: contig of 17042 bp in length
            *    57618    57717: gap of unknown length
            *    57718    75708: contig of 17991 bp in length
            *    75709    75808: gap of unknown length
            *    75809    89018: contig of 13210 bp in length
            *    89019    89118: gap of unknown length
            *    89119   100348: contig of 11230 bp in length
            *   100349   100448: gap of unknown length
            *   100449   110704: contig of 10256 bp in length
            *   110705   110804: gap of unknown length
            *   110805   123156: contig of 12352 bp in length
            *   123157   123256: gap of unknown length
            *   123257   132467: contig of 9211 bp in length
            *   132468   132567: gap of unknown length
            *   132568   141461: contig of 8894 bp in length
            *   141462   141561: gap of unknown length
            *   141562   146576: contig of 5015 bp in length
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            *   146677   151201: contig of 4525 bp in length
            *   151202   151301: gap of unknown length
            *   151302   155722: contig of 4421 bp in length
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            *   155823   160148: contig of 4326 bp in length
            *   160149   160248: gap of unknown length
            *   160249   163024: contig of 2776 bp in length
            *   163025   163124: gap of unknown length
            *   163125   165339: contig of 2215 bp in length
            *   165340   165439: gap of unknown length
            *   165440   168113: contig of 2674 bp in length
            *   168114   168213: gap of unknown length
            *   168214   169867: contig of 1654 bp in length
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FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             41.2%;  Score 528;  DB 2;  Length 175826;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-120;
  Matches  528;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        743 AGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGT 802
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Db      83982 AGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGT 84041

Qy        803 CATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATT 862
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Db      84042 CATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATT 84101

Qy        863 TATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGG 922
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Db      84102 TATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGG 84161

Qy        923 GGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGA 982
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Db      84162 GGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGA 84221

Qy        983 CAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGG 1042
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Db      84222 CAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGG 84281

Qy       1043 AGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCA 1102
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Db      84282 AGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCA 84341

Qy       1103 AAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCC 1162
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Db      84342 AAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCC 84401

Qy       1163 CCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAA 1222
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Qy       1223 GAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACA 1270
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Db      84462 GAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACA 84509


RESULT 9
AL451085/c
LOCUS       AL451085              182166 bp    DNA     linear   PRI 09-MAR-2002
DEFINITION  Human DNA sequence from clone RP11-307C12 on chromosome 1, complete
            sequence.
ACCESSION   AL451085 AC027440
VERSION     AL451085.20  GI:19309454
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 182166)
  AUTHORS   Brown,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAR-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
```

```
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Mar 8, 2002 this sequence version replaced gi:19031396.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
            Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr1
            RP11-307C12 is from the library RPCI-11.2 constructed by the group
            of Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6
            This sequence is the entire insert of clone RP11-307C12 The true
            right end of clone RP11-196D4 is at 89714 in this sequence.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
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                     by restriction digest."
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                     by restriction digest."
ORIGIN

  Query Match             41.2%;  Score 528;  DB 9;  Length 182166;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-120;
  Matches  528;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        743 AGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGT 802
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Db      53705 AGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGT 53646

Qy        803 CATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATT 862
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Db      53645 CATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATT 53586

Qy        863 TATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGG 922
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Db      53585 TATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGG 53526

Qy        923 GGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGA 982
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Qy        983 CAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGG 1042
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Qy        1043 AGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCA 1102
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Db       53405 AGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCA 53346

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Db       53345 AAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCC 53286

Qy        1163 CCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAA 1222
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Db       53285 CCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAA 53226

Qy        1223 GAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACA 1270
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Db       53225 GAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACA 53178

RESULT 10
AC034149/c
LOCUS       AC034149              195189 bp    DNA     linear   HTG 01-SEP-2000
DEFINITION  Homo sapiens chromosome 1 clone RP11-163D16, WORKING DRAFT
            SEQUENCE, 11 unordered pieces.
ACCESSION   AC034149
VERSION     AC034149.3  GI:9958177
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 195189)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 195189)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-APR-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Sep 1, 2000 this sequence version replaced gi:7579855.

            ----------------- Genome Center -----------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            -------------- Project Information --------------
            Center project name: H_NH0163D16
            -------------- Summary Statistics  --------------
            Sequencing vector: M13; 100%
            Sequencing vector: plasmid; 0%
            Chemistry: Dye-primer ET; 100% of reads
            Chemistry: Dye-terminator Big Dye; 0% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 189877 bases at least Q40
            Consensus quality: 191604 bases at least Q30
            Consensus quality: 192567 bases at least Q20
            Insert size: 178000; agarose-fp
            Insert size: 194189; sum-of-contigs
            Quality coverage: 6.28 in Q20 bases; agarose-fp
            Quality coverage: 5.78 in Q20 bases; sum-of-contigs
            -------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 11 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1     2708: contig of 2708 bp in length
            *    2709     2808: gap of unknown length
            *    2809     6955: contig of 4147 bp in length
            *    6956     7055: gap of unknown length
            *    7056    14453: contig of 7398 bp in length
            *   14454    14553: gap of unknown length
            *   14554    23402: contig of 8849 bp in length
            *   23403    23502: gap of unknown length
            *   23503    37767: contig of 14265 bp in length
            *   37768    37867: gap of unknown length
            *   37868    54470: contig of 16603 bp in length
            *   54471    54570: gap of unknown length
            *   54571    82102: contig of 27532 bp in length
            *   82103    82202: gap of unknown length
            *   82203   118832: contig of 36630 bp in length
            *  118833   118932: gap of unknown length
            *  118933   191118: contig of 72186 bp in length
            *  191119   191218: gap of unknown length
            *  191219   192795: contig of 1577 bp in length
            *  192796   192895: gap of unknown length
            *  192896   195189: contig of 2294 bp in length.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /chromosome="1"
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     misc_feature    2809..6955
                     /note="assembly_name:Contig11"
     misc_feature    7056..14453
                     /note="assembly_name:Contig12"
     misc_feature    14554..23402
                     /note="assembly_name:Contig13"
     misc_feature    23503..37767
                     /note="assembly_name:Contig14"
     misc_feature    37868..54470
                     /note="assembly_name:Contig15
                     clone_end:T7
                     vector_side:right"
     misc_feature    54571..82102
                     /note="assembly_name:Contig16"
     misc_feature    82203..118832
                     /note="assembly_name:Contig17"
     misc_feature    118933..191118
                     /note="assembly_name:Contig18"
     misc_feature    191219..192795
                     /note="assembly_name:Contig8"
     misc_feature    192896..195189
                     /note="assembly_name:Contig9
                     clone_end:SP6
                     vector_side:left"
ORIGIN

  Query Match             41.2%;  Score 528;  DB 2;  Length 195189;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-120;
  Matches  528;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         743 AGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGT 802
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Db      134351 AGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGT 134292

Qy         803 CATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATT 862
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      134291 CATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATT 134232

Qy         863 TATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGG 922
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      134231 TATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGG 134172

Qy         923 GGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGA 982
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134171 GGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGA 134112

Qy        983 CAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGCAAGGCAGGAAACCTCTGG 1042
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Db     134111 CAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGCAAGGCAGGAAACCTCTGG 134052

Qy       1043 AGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCA 1102
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Db     134051 AGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCA 133992

Qy       1103 AAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCC 1162
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Db     133991 AAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCC 133932

Qy       1163 CCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAA 1222
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Db     133931 CCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAA 133872

Qy       1223 GAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACA 1270
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db     133871 GAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACA 133824


RESULT 11
AX886270
LOCUS       AX886270                 465 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 2133 from Patent EP1033401.
ACCESSION   AX886270
VERSION     AX886270.1  GI:40043263
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
  TITLE     Expressed sequence tags and encoded human proteins
  JOURNAL   Patent: EP 1033401-A 2133 06-SEP-2000;
            Genset (FR)
FEATURES             Location/Qualifiers
     source          1..465
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             57..>464
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAF00408.1"
                     /db_xref="GI:40043264"
                     /translation="MAPLGGAPRLVLLFSXKRKSGKDFVTZALQSRLGADVCAVLRLS
                     GPLKEQYAQEHGLNFQRLLDTSTYKEAFRKDMIRWGEEKRQAXXGFFCRKIVEGISQP
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ORIGIN

  Query Match             35.8%;  Score 459.2;  DB 6;  Length 465;
  Best Local Similarity   98.5%;  Pred. No. 5.1e-103;
  Matches  458;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        247 GATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGG 306
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Db          1 GATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGG 60

Qy        307 CCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGA 366
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db         61 CCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGRCAAGAGGAAATCCGGGA 120

Qy        367 AGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCC 426
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Db        121 AGGACTTCGTGACCSAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCC 180

Qy        427 GGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGAC 486
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Db        181 GGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGAC 240
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Qy        487 TCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGAGAGG 546
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Db        241 TCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGAGAGG 300

Qy        547 AGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGC 606
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Db        301 AGAAACGCCAGGCTGNNNCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGC 360

Qy        607 CCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAGGCCT 666
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Db        361 CCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGARGCCT 420

Qy        667 ATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGA 711
              |||||||||||||||||||||||||||||||||||||||||| ||
Db        421 ATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCGGA 465


RESULT 12
BD025880
LOCUS       BD025880                 465 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Sequence tag and encoded human protein.
ACCESSION   BD025880
VERSION     BD025880.1  GI:22567103
KEYWORDS    JP 2001269182-A/2126.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 465)
  AUTHORS   Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
  TITLE     Sequence tag and encoded human protein
  JOURNAL   Patent: JP 2001269182-A 2126 02-OCT-2001;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001269182-A/2126
            PD   02-OCT-2001
            PF   24-FEB-2000 JP 2000118773
            PR   26-FEB-1999 US    60/122487
            PI   JEAN BAPUTIST DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
            PI   JORDAN
            PC   C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
             G06F15/40
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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
ORIGIN

  Query Match             35.8%;  Score 459.2;  DB 6;  Length 465;
  Best Local Similarity   98.5%;  Pred. No. 5.1e-103;
  Matches  458;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        247 GATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGG 306
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Db          1 GATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGG 60

Qy        307 CCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGA 366
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db         61 CCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGRCAAGAGGAAATCCGGGA 120

Qy        367 AGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCC 426
              ||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGACTTCGTGACCSAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCC 180

Qy        427 GGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGAC 486
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Db          181 GGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGAC 240

Qy          487 TCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGAGAGG 546
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Db          241 TCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGAGAGG 300

Qy          547 AGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGC 606
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Db          301 AGAAACGCCAGGCTGNNNCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGC 360

Qy          607 CCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAGGCCT 666
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Db          361 CCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGARGCCT 420

Qy          667 ATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGA 711
                |||||||||||||||||||||||||||||||||||||||||| ||
Db          421 ATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCGGA 465

RESULT 13
BC028659
LOCUS       BC028659                1008 bp    mRNA    linear   ROD 06-OCT-2003
DEFINITION  Mus musculus RIKEN cDNA 1110011E12 gene, mRNA (cDNA clone MGC:41584
            IMAGE:1247653), complete cds.
ACCESSION   BC028659
VERSION     BC028659.1  GI:20306533
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1008)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1008)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-APR-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Marcello Bento  Soares, Ph.D.
            cDNA Library Preparation: M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 66 Row: h Column: 3.
FEATURES             Location/Qualifiers
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                     /db_xref="GI:20306534"
                     /db_xref="LocusID:68603"
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                     EAYGAVIQTVRVVASEQSRQQRGWVFTPGVDDAESECGLDNFGNFDWVIENHGDEQCL
                     EDQLEHLLGFIQAKL"
     misc_feature    266..427
                     /note="P-mevalo_kinase; Region: Phosphomevalonate kinase.
                     Phosphomevalonate kinase (EC:2.7.4.2) catalyzes the
                     phosphorylation of 5-phosphomevalonate into
                     5-diphosphomevalonate, an essential step in isoprenoid
                     biosynthesis via the mevalonate pathway. This family
                     represents the animal type of the enzyme. The other is the
                     ERG8 type, found in plants and fungi, and some bacteria
                     (see pfam00288)"
                     /db_xref="CDD:pfam04275"
ORIGIN

  Query Match             28.1%;  Score 359.6;  DB 10;  Length 1008;
  Best Local Similarity   72.4%;  Pred. No. 2.7e-78;
  Matches  552;  Conservative    0;  Mismatches  194;  Indels   16;  Gaps    6;

Qy          456 GCTCAGGAGCATGGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCC 515
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Db          194 GCAAAGGAGCATGGCTTGGACTTCCAGAGACTTCTGGATGCGAGCACCTACAAGGAGACC 253

Qy          516 TTTCGGAAGGACATGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTT 575
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Db          254 TATCGGAGGGACATGATCTGTTGGGGGAGCAGAAGCGCCAGGCAGACCCAGGCTTCTTC 313

Qy          576 TGCAGGAAGATTGTGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGA 635
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Db          314 TGCCGGAAGATTGTGGAAGGCGTGTCCCAGCCTATCTGGCTGGTGAGTGACACACGGAGG 373

Qy          636 GTGTCTGACATCCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTT 695
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Db          374 ACATCTGACATCCAGTGGTTTCAGGAGGCCTATGGGGCTGTGATACAGACAGTCCGAGTA 433

Qy          696 GTAGCGTTGGAGCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGAT 755
                || || | ||||||||| |||||||| ||||||||||||||||| |||||||||||||||
Db          434 GTGGCCTCGGAGCAGAGTCGACAGCAACGGGGCTGGGTGTTCACACCAGGGGTGGACGAT 493

Qy          756 GCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCAT 815
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Qy          816 GGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGA 875
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Db          554 GGAGATGAGCAGTGCCTGGAGGATCAGCTGGAGCACCTGCTGGGATTTATTCAAGCCAAA 613

Qy          876 CTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACT 935
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Db        614 CTTTAGTGATGAGGCTTGAGGGACGAGCAGAGACTGATGGCCTGGCGAACAG-TGGTT 672

Qy        936 CTGCAAAATGGGGGTGTCCC--CCGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTC 993
              |||| | ||| ||||  ||   || | ||  |   ||   |   ||||||||   || |
Db        673 CTGCCAGATGTGGGTCCCCAGTCCCAGCCGAGGTCAGCAAACAGACAGACAGTCTGGCTT 732

Qy        994 TAGA------TTCTGAGGGGGTTGGTGGATATTGGCAAGGCAGGAAACCTCTGGAGACC 1047
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Db        733 GCCAGAGGTCTGGGCAGGATGCTCGTGAGTAGTGGGCAAATAAAGAAACCTCTGGTG--- 789

Qy       1048 TCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCAAAGGA 1107
              |  | || ||| ||| || ||||  |   ||||| |||     |||  ||||||||||
Db        790 TTGTGTTTTCCCTGGAGAGGACACTCTGCCTCTTTAGGGC---ACTTATAGGGCAAAGGC 846

Qy       1108 GGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCCCCTCA 1167
               || |  |  | | ||| ||| |  | |||  ||||| | ||    ||      |
Db        847 AGGCGCATGAGTTTTGCCTGAGGCAGGAACATTGCCACACCCATGATGGGCAGGCTGCAG 906

Qy       1168 GCCTGTGGTGGCCTTGCAT-CCTGACTGGATGTTCTCAGCCC 1208
                ||||| |||   ||  | ||||  || | | |||||||||
Db        907 AGCTGTGATGGTGGTGTTTCCCTGTGTGTACGCTCTCAGCCC 948

RESULT 14
G22398/c
LOCUS       G22398                   422 bp    DNA     linear   STS 31-MAY-1996
DEFINITION  human STS WI-14846, sequence tagged site.
ACCESSION   G22398
VERSION     G22398.1  GI:1342724
KEYWORDS    STS; STS sequence; primer; sequence tagged site.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 422)
  AUTHORS   Hudson,T.
  TITLE     Whitehead Institute/MIT Center for Genome Research; Physically
            Mapped STSs
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Thomas Hudson
            Whitehead Institute/MIT Center for Genome Research
            Whitehead Institute for Biomedical Research
            9 Cambridge Center, Cambridge MA 02142 USA
            Tel: 617 252 1900
            Fax: 617 252 1902
            Email: thudson@genome.wi.mit.edu

            Primer A: AGGTTTATTAGTATCCACACTGGG
            Primer B: TGTCTTGGCTGTGCTTGAAG
            STS size: 150
            PCR Profile:
                  Presoak:
                  Denaturation:
                  Annealing: 56 degrees C
                  Polymerization:
                  PCR Cycles: 35
                  Thermal Cycler:
            Protocol:
                Template: 10 ng
                Primer: each 5 pM
                dNTPs: each 4 nM
                Taq Polymerase: 0.025 units/ul
                Total Vol: 20 ul

            Buffer:
                MgCl2: 1.5 mM
                KCl: 50 mM
                Tris-HCL: 10 mM
                pH: 9.3

            Derived from dbEST (genbank accession H09819).
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FEATURES             Location/Qualifiers
     source          1..422
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="730.7 cR from top of Chr1 linkage group"
     STS             23..172
     primer_bind     23..46
     primer_bind     complement(153..172)
ORIGIN

  Query Match             26.0%;  Score 333.6;  DB 11;  Length 422;
  Best Local Similarity   97.0%;  Pred. No. 7.7e-72;
  Matches  360;  Conservative    0;  Mismatches    9;  Indels    2;  Gaps    2;

Qy        913 CTGAGGTGGGGGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGT 972
              || |||||||||||||||||||||||||||||||||    ||||    ||||||||||||
Db        371 CTNAGGTGGGGGTGGGGCTGACTCTGCAAAATGGGGTGTCCCCCGATCCCTGGCCGAGGT 312

Qy        973 GAGGAACAGACAGGGGGGGT-CTAGATTCTGAGGGGGTTGGTGGATATTGGCAAGGCAG 1031
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        311 GAGGAACAGACAGGGGGGGTNCTAGATTCTGAGGGGGTTGGTGGATATTGGCAAGGCAG 252

Qy       1032 GAAACCTCTGGAGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGA 1091
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 GAAACCTCTGGAGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGA 192

Qy       1092 CTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCC 1151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 CTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCC 132

Qy       1152 AGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTT 1211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 AGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTT 72

Qy       1212 GTT-CTGGGCAAGAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACA 1270
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 GTTCCTGGGCAAGAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACA 12

Qy       1271 AAAAAAAAAAA 1281
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Db         11 AAAAAAAAAAA 1

RESULT 15
AR415566
LOCUS       AR415566                 419 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 3203 from patent US 6639063.
ACCESSION   AR415566
VERSION     AR415566.1  GI:40170676
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 419)
  AUTHORS   Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
  TITLE     EST's and encoded human proteins
  JOURNAL   Patent: US 6639063-A 3203 28-OCT-2003;
FEATURES             Location/Qualifiers
     source          1..419
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                     /mol_type="genomic DNA"
ORIGIN

  Query Match             24.8%;  Score 317.2;  DB 6;  Length 419;
  Best Local Similarity   85.6%;  Pred. No. 9e-68;
  Matches  416;  Conservative    0;  Mismatches    3;  Indels   67;  Gaps    3;

Qy        229 CATTCCGCGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGA 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CATTCCGCGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGA 60

Qy        289 GGCGTGGCGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCG 348
```

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              |||||||||||||||||||||     ||||||||||||||||||||||||||||||||||
Db         61 GGCGTGGCGGCCCCATGGCCC--GCTGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCG 118

Qy        349 GCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTG 408
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        119 GCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAG-------------- 164

Qy        409 ATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATG 468
                                                                ||||||||||
Db        165 --------------------------------------------------CAGGAGCATG 174

Qy        469 GCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACA 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 GCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACA 234

Qy        529 TGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTG 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 TGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTG 294

Qy        589 TGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCC 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 TGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCC 354

Qy        649 AGTGGTTTCGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGC 708
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        355 AGTGGTTTCGGAGGCCTATGGGG-CGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGC 413

Qy        709 AGAGCC 714
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Db        414 AGAGCC 419

Search completed: March 11, 2004, 03:35:24
Job time : 3271.98 secs
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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2004  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         March  7, 2004, 05:45:58 ; Search time 28647 Seconds
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                                           11793.868 Million cell updates/sec

Title:          US-10-084-817-2
Perfect score:  7795
Sequence:       1 cggctcgagccggctgtgct..........ttttaaatatccacagtact 7795

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters:      6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
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       Pred. No. is the number of results predicted by chance to have a
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         score greater than or equal to the score of the result being printed,
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     2    7773.2      99.7    8042  9  HSM806805              BX640731 Homo sapi
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     4    7760.4      99.6    8035  9  HSM806171              BX538018 Homo sapi
     5    7562.4      97.0    7951  9  HSM806901              BX640802 Homo sapi
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    17    7413.4      95.1    7705  6  AR364992               AR364992 Sequence
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    19      7372      94.6    8421  9  HSM806903              BX640803 Homo sapi
    20      7223      92.7    7803  6  AR051657               AR051657 Sequence
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    22    6680.8      85.7    7544  9  HSM803509              AL832202 Homo sapi
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    25    5320.6      68.3    8329  6  AX402055               AX402055 Sequence
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    27    4213.6      54.1    4488  9  HSM807064              BX640920 Homo sapi
    28    3274.8      42.0    3818  9  HSM806684              BX640638 Homo sapi
    29      3078      39.5    8216  5  XELFBRNCT              M77820 Xenopus lae
    30    2823.8      36.2    4435 10   MMFIBL                 X93167 M.musculus
    31    2361.8      30.3    9157  9  HSM807163              BX641150 Homo sapi
    32    2211.8      28.4    4027  6  AR051659               AR051659 Sequence
    33    2201.6      28.2    4321  9  HSM806214              BX538045 Homo sapi
    34    2194.2      28.1    3059 10   BC051082               BC051082 Mus muscu
    35    2178.4      27.9    2384  9  HUMFNC                 M10905 Human cellu
    36    2068.2      26.5    8267  5  AF081128               AF081128 Danio rer
    37    1992.2      25.6    2192  9  HSA535086              AJ535086 Homo sapi
    38    1976.6      25.4    2348  6  AX397512               AX397512 Sequence
    39    1976.6      25.4    2348  9  HSU42594               U42594 Human fibro
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    43    1887.4      24.2    2147  9  HSA276395              AJ276395 Homo sapi
    44    1837.2      23.6    3141 10   BC025521               BC025521 Mus muscu
    45    1787.4      22.9    3618  5  GGU21327               U21327 Gallus gall


                                  ALIGNMENTS


RESULT 1
AX281712
LOCUS       AX281712                8044 bp    DNA     linear   PAT 02-NOV-2001
DEFINITION  Sequence 121 from Patent WO0177389.
ACCESSION   AX281712
VERSION     AX281712.1  GI:16608963
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shiffman,D., Somogyi,R., Lawn,R., Seilhamer,J.J., Porter,G.J.,
            Mikita,T. and Tai,J.
  TITLE     Genes expressed in foam cell differentiation
  JOURNAL   Patent: WO 0177389-A 121 18-OCT-2001;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .8044
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                     /db_xref="taxon:9606"
                     /note="Incyte ID No: 427813.14"
ORIGIN

  Query Match             99.8%;  Score 7780.6;  DB 6;  Length 8044;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7786;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 CGGCTCGAGCCGGCTGTGCTGCACAGGGGGAGGAGAGGGAACCCCAGGCGCGAGCGGGAA 60
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Db          1 CGGCTCGAGCCGGCTGTGCTGCACAGGGGGAGGAGAGGGAACCCCAGGCGCGAGCGGGAA 60

Qy         61 GAGGGGACCTGCAGCCACAACTTCTCTGGTCCTCTGCATCCCTTCTGTCCCTCCACCCGT 120
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Db         61 GAGGGGACCTGCAGCCACAACTTCTCTGGTCCTCTGCATCCCTTCTGTCCCTCCACCCGT 120

Qy        121 CCCCTTCCCCACCCTCTGGCCCCCACCTTCTTGGAGGCGACAACCCCCGGGAGGCATTAG 180
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Qy        181 AAGGGATTTTTCCCGCAGGTTGCGAAGGGAAGCAAACTTGGTGGCAACTTGCCTCCCGGT 240
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Qy        241 GCGGGCGTCTCTCCCCCACCGTCTCAACATGCTTAGGGGTCCGGGGCCCGGGCTGCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCGGGCGTCTCTCCCCCACCGTCTCAACATGCTTAGGGGTCCGGGGCCCGGGCTGCTGCT 300

Qy        301 GCTGGCCGTCCTGTGCCTGGGGACAGCGGTGCCCTCCACGGGAGCCTCGAAGAGCAAGAG 360
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Db        301 GCTGGCCGTCCTGTGCCTGGGGACAGCGGTGCCCTCCACGGGAGCCTCGAAGAGCAAGAG 360

Qy        361 GCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCGG 420

Qy        421 TTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGG 480

Qy        481 CAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAACC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
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Qy        541 TGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACAC 600
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Db        541 TGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACAC 600

Qy        601 TTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGCGAGG 660
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        601 TTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATTGGGGCTGGCGAGG 660

Qy        661 GAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGG 720
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Db        661 GAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGG 720

Qy        721 TGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTGTGTGTGTCTTGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTGTGTGTGTCTTGG 780

Qy        781 TAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGC 840

Qy        841 TGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGT 900
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Qy        901 AGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATG 960

Qy        961 CAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAA 1020

Qy       1021 TCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGA 1080
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Db       1021 TCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGA 1080

Qy       1081 GAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTGC 1140
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Db       1081 GAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTGC 1140

Qy       1141 AGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCACTGTGTCACAGA 1200
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Qy       1261 GCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGTAACCCAGACTTA 1320
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Qy       1321 CGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAATGGCAGGACGTT 1380
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Qy       1381 CTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAGCACAACTTCGAA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAGCACAACTTCGAA 1440

Qy       1441 TTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTTGGTTCAGACTCG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1501 AGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAACAACCACAATTA 1560
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGAGGAAATCTGCAC 1680

Qy       1681 AACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCAGCATGACATGGG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 AACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCAGCATGACATGGG 1740

Qy       1741 TCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGACATGCATTGCCTA 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGACATGCATTGCCTA 1800

Qy       1801 CTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATT 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATT 1860

Qy       1861 CCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGG 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGG 1920

Qy       1921 CAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCA 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCA 1980
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y    1981 AATTGGAGATTCATGGAGAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGG 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    1981 AATTGGAGATTCATGGAGAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGG 2040

y    2041 CCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2041 CCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCC 2100

y    2101 TGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2101 TGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAA 2160

y    2161 TGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2161 TGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGT 2220

y    2221 AGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2221 AGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCT 2280

y    2281 GAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2281 GAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGA 2340

y    2341 AGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGACCAGCAACACCGT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2341 AGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGACCAGCAACACCGT 2400

y    2401 GACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAAT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2401 GACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAAT 2460

y    2461 CACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2461 CACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCG 2520

y    2521 GGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCAC 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2521 GGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCAC 2580

y    2581 AGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2581 AGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTA 2640

y    2641 TCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2641 TCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCC 2700

y    2701 TGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2701 TGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTG 2760

y    2761 GAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2761 GAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGG 2820

y    2821 TAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCA 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2821 TAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCA 2880

y    2881 ACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2881 ACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACC 2940

y    2941 TGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAG 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2941 TGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAG 3000

y    3001 GGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    3001 GGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGA 3060

y    3061 GAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGG 3120
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 GAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGG 3120

Qy   3121 GCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGT 3180

Qy   3181 CACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGC 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 CACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGC 3240

Qy   3241 TCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTC 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTC 3300

Qy   3301 TACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGT 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 TACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGT 3360

Qy   3361 GGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTA 3420
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   3361 GGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTA 3420

Qy   3421 CCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGG 3480
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 CCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGG 3480

Qy   3481 CAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTAT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTAT 3540

Qy   3541 TCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCC 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCC 3600

Qy   3601 AAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 AAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGT 3660

Qy   3661 GACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTA 3720

Qy   3721 CACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGT 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 CACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGT 3780

Qy   3781 GACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCT 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCT 3840

Qy   3841 CACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAAC 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 CACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAAC 3900

Qy   3901 CCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTC 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 CCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTC 3960

Qy   3961 CTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAA 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAA 4020

Qy   4021 GGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCAC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 GGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCAC 4080

Qy   4081 TGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCC 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 TGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCC 4140

Qy   4141 ATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGT 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 b     4141 ATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGT 4200

 y     4201 TGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGG 4260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 b     4201 TGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGG 4260

 y     4261 TACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAG 4320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 b     4261 TACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAG 4320

 y     4321 AGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGC 4380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 b     4321 AGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGC 4380

 y     4381 CAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCG 4440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 b     4381 CAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCG 4440

 y     4441 CCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAA 4500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 b     4441 CCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAA 4500

 y     4501 TTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCT 4560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 b     4501 TTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCT 4560

 y     4561 TAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCC 4620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 b     4561 TAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCC 4620

 y     4621 GAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCC 4680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 b     4621 GAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCC 4680

 y     4681 TGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGT 4740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 b     4681 TGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGT 4740

 y     4741 CCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGG 4800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 b     4741 CCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGG 4800

 y     4801 AGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAG 4860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 b     4801 AGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAG 4860

 y     4861 CAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGAC 4920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 b     4861 CAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGAC 4920

 y     4921 CGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGG 4980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 b     4921 CGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGG 4980

 y     4981 TTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGG 5040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4981 TTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGG 5040

Qy     5041 TCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAG 5100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5041 TCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAG 5100

Qy     5101 TGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAA 5160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5101 TGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAA 5160

Qy     5161 CATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGC 5220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5161 CATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGC 5220

Qy     5221 TTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGA 5280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5221 TTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGA 5280
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Qy     5281 TGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGG 5340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5281 TGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGG 5340

Qy     5341 CCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAG 5400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5341 CCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAG 5400

Qy     5401 CCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCAC 5460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5401 CCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCAC 5460

Qy     5461 TCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGG 5520
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5461 TCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGG 5520

Qy     5521 ATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGC 5580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5521 ATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGC 5580

Qy     5581 TCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAG 5640
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5581 TCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAG 5640

Qy     5641 TGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTGTCACCACTCT 5700
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     5641 TGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGTTGTCACCACTCT 5700

Qy     5701 GGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCAC 5760
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5701 GGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCAC 5760

Qy     5761 CATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGATGCCGTTCCAGC 5820
            ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db     5761 CATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGC 5820

Qy     5821 CAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCAC 5880
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5821 CAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCAC 5880

Qy     5881 TGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCG 5940
             || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5881 AGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCG 5940

Qy     5941 GAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTT 6000
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5941 GAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTT 6000

Qy     6001 CCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTAC 6060
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6001 CCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTAC 6060

Qy     6061 CGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCC 6120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6061 CGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCC 6120

Qy     6121 CCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAAT 6180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6121 CCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAAT 6180

Qy     6181 TTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGAC 6240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6181 TTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGAC 6240

Qy     6241 AGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTT 6300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6241 AGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTT 6300

Qy     6301 GGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGG 6360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6301 GGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGG 6360
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Qy       6361 AAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGAT 6420
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Db       6361 AAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGAT 6420

Qy       6421 CTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCA 6480
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Qy       6481 TAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTC 6540
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Qy       6541 ATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTGTTGGCACTGA 6600
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Qy       6661 CACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAA 6720
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Qy       6721 GGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTAC 6780
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Qy       6841 ACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCA 6900
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Qy       6901 TTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGA 6960
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Qy       6961 GAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTCTTGGGAACGG 7020
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Qy       7021 AAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGATGGGAAGACATA 7080
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Qy       7081 CCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTT 7140
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Qy       7141 TGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGGTGAACCCAGTCC 7200
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Qy       7201 CGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCATCAGAGAACAAA 7260
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Qy       7321 AGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCTCTCTGCCAAG 7380
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Qy       7621 TCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGATATGACCAAA 7680
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Qy       7741 ACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCACAGTACT 7795
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RESULT 2
HSM806805
LOCUS       HSM806805               8042 bp    mRNA    linear   PRI 28-AUG-2003
DEFINITION  Homo sapiens mRNA; cDNA DKFZp686M2451 (from clone DKFZp686M2451);
            complete cds.
ACCESSION   BX640731
VERSION     BX640731.1  GI:34364819
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8042)
  AUTHORS   Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  CONSRTM   The German Human cDNA Consortium
  TITLE     Direct Submission
  JOURNAL   Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by DKFZ (German Cancer Research Center,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp686M2451) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.
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RIGIN

  Query Match             99.7%;  Score 7773.2;  DB 9;  Length 8042;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7781;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          2 GGCTCGAGCCGGCTGTGCTGCACAGGGGGAGGAGAGGGAACCCCAGGCGCGAGCGGGAAG 61
              ||| || |||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         62 AGGGGACCTGCAGCCACAACTTCTCTGGTCCTCTGCATCCCTTCTGTCCCTCCACCCGTC 121
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Db         61 AGGGGACCTGCAGCCACAACTTCTCTGGTCCTCTGCATCCCTTCTGTCCCTCCACCCGTC 120

Qy        122 CCCTTCCCCACCCTCTGGCCCCCACCTTCTTGGAGGCGACAACCCCCGGGAGGCATTAGA 181
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Db        121 CCCTTCCCCACCCTCTGGCCCCCACCTTCTTGGAGGCGACAACCCCCGGGAGGCATTAGA 180

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Qy        242 CGGGCGTCTCTCCCCCACCGTCTCAACATGCTTAGGGGTCCGGGGCCCGGGCTGCTGCTG 301
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Qy        362 CAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCGGT 421
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Qy        602 TATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGG 661
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Qy        662 AGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGGT 721
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Qy        782 AATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGCT 841
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Qy       1382 TACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAGCACAACTTCGAAT 1441
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Qy       1802 TCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATTC 1861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATTC 1860

Qy       1862 CACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGC 1921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGC 1920

Qy       1922 AGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCAA 1981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 AGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCAA 1980

Qy       1982 ATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGC 2041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 ATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGC 2040

Qy       2042 CGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCCT 2101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCCT 2100

Qy       2102 GTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAAT 2161
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAAT 2160

Qy       2162 GCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTA 2221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 GCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTA 2220

Qy       2222 GGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTG 2281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 GGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTG 2280

Qy       2282 AAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAA 2341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 AAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAA 2340

Qy       2342 GTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGACCAGCAACACCGTG 2401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 GTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGACCAGCAACACCGTG 2400

Qy       2402 ACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATC 2461
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 ACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATC 2460

Qy       2462 ACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGG 2521
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 ACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGG 2520

Qy       2522 GTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACA 2581
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACA 2580

Qy       2582 GCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTAT 2641
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTAT 2640

Qy       2642 CAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCCT 2701
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCCT 2700

Qy       2702 GATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGG 2761
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GATGCCCCACCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGG 2760

Qy       2762 AGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGT 2821
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 AGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGT 2820

Qy       2822 AGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAA 2881
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 AGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAA 2880

Qy       2882 CCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCT 2941
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 CCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCT 2940

Qy       2942 GTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGG 3001
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 GTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGG 3000

Qy       3002 GACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAG 3061
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 GACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAG 3060

Qy       3062 AGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGG 3121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 AGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGG 3120

Qy       3122 CAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTC 3181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 CAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTC 3180

Qy       3182 ACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCT 3241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 ACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCT 3240

Qy       3242 CAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCT 3301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 CAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCT 3300

Qy       3302 ACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGTG 3361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 ACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGTG 3360

Qy       3362 GGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTAC 3421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 GGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTAC 3420

Qy       3422 CCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGC 3481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 CCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGC 3480

Qy       3482 AACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATT 3541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 AACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATT 3540

Qy       3542 CCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCCA 3601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 CCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCCA 3600

Qy       3602 AGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTG 3661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 AGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTG 3660

Qy       3662 ACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTAC 3721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 ACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTAC 3720

Qy       3722 ACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTG 3781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 ACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTG 3780

Qy       3782 ACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTC 3841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 ACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTC 3840

Qy       3842 ACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACC 3901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 ACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACC 3900

Qy       3902 CCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCC 3961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 CCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCC 3960

Qy       3962 TGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAG 4021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 TGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAG 4020

Qy       4022 GATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCACT 4081
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 GATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCACT 4080

Qy       4082 GACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCCA 4141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 GACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCCA 4140

Qy       4142 TCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGTT 4201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 TCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGTT 4200

Qy       4202 GCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGGT 4261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 GCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGGT 4260

Qy       4262 ACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGA 4321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 ACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGA 4320

Qy       4322 GGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGCC 4381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 GGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGCC 4380

Qy       4382 AACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGC 4441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 AACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGC 4440

Qy       4442 CATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAAT 4501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 CATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAAT 4500

Qy       4502 TCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCTT 4561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 TCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCTT 4560

Qy       4562 AATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCG 4621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 AATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCG 4620

Qy       4622 AGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCCT 4681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 AGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCCT 4680
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Qy       4682 GCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGTC 4741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 GCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGTC 4740

Qy       4742 CAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGGA 4801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 CAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGGA 4800

Qy       4802 GTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGC 4861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 GTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGC 4860

Qy       4862 AAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACC 4921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 AAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACC 4920

Qy       4922 GATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGT 4981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 GATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGT 4980

Qy       4982 TACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGGT 5041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 TACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGGT 5040

Qy       5042 CCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAGT 5101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 CCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAGT 5100

Qy       5102 GTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAAC 5161
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 GTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAAC 5160

Qy       5162 ATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGCT 5221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 ATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGCT 5220

Qy       5222 TGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGAT 5281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 TGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGAT 5280

Qy       5282 GGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGC 5341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5281 GGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGC 5340

Qy       5342 CTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAGC 5401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5341 CTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAGC 5400

Qy       5402 CAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCACT 5461
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db       5401 CAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAGCTGACCTGAAGTTCACT 5460

Qy       5462 CAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGGA 5521
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5461 CAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGGA 5520

Qy       5522 TATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCT 5581
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5521 TATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCT 5580

Qy       5582 CCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAGT 5641
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5581 CCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAGT 5640

Qy       5642 GTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTGTCACCACTCTG 5701
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db       5641 GTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGTTGTCACCACTCTG 5700

Qy       5702 GAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACC 5761
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5701 GAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACC 5760
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y         5762 ATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGATGCCGTTCCAGCC 5821
               |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
b         5761 ATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCC 5820

y         5822 AATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACT 5881
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         5821 AATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACA 5880

y         5882 GGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGG 5941
               || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         5881 GGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGG 5940

y         5942 AGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTC 6001
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         5941 AGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTC 6000

y         6002 CTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACC 6061
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         6001 CTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACC 6060

y         6062 GGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCC 6121
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         6061 GGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCC 6120

y         6122 CGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATT 6181
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         6121 CGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATT 6180

y         6182 TATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACA 6241
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         6181 TATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACA 6240

y         6242 GACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTTG 6301
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         6241 GACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTTG 6300

y         6302 GATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGGA 6361
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         6301 GATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGGA 6360

y         6362 AATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGATC 6421
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         6361 AATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGATC 6420

y         6422 TTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCAT 6481
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         6421 TTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCAT 6480

y         6482 AGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTCA 6541
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         6481 AGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTCA 6540

y         6542 TGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTGTTGGCACTGAT 6601
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y         6602 GAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTCTGACAGGCCTC 6661
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b         6601 GAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTCTGACAGGCCTC 6660

y         6662 ACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAAG 6721
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b         6661 ACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAAG 6720

y         6722 GTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACG 6781
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y         6782 GATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGGAGATGAGTGGGAA 6841
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Qy        7082 CACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTTT 7141
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Qy        7322 GATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCTCTCTGCCAAGA 7381
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Qy        7562 CGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATTTGGTTTGGGAT 7621
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RESULT 3
HSM806170
LOCUS       HSM806170               8030 bp    mRNA    linear   PRI 17-JUN-2003
DEFINITION  Homo sapiens mRNA; cDNA DKFZp686O016 (from clone DKFZp686O016).
ACCESSION   BX538017
VERSION     BX538017.1  GI:31874108
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8030)
  AUTHORS   Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by EMBL (European Molecular Biology Laboratories,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp686O016) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             99.6%;  Score 7760.4;  DB 9;  Length 8030;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 7773;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          2 GGCTCGAGCCGGCTGTGCTGCACAGGGGGAGGAGAGGGAACCCCAGGCGCGAGCGGGAAG 61
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Qy         62 AGGGGACCTGCAGCCACAACTTCTCTGGTCCTCTGCATCCCTTCTGTCCCTCCACCCGTC 121
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Qy        122 CCCTTCCCCACCCTCTGGCCCCCACCTTCTTGGAGGCGACAACCCCCGGGAGGCATTAGA 181
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Qy        182 AGGGATTTTTCCCGCAGGTTGCGAAGGGAAGCAAACTTGGTGGCAACTTGCCTCCCGGTG 241
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y      902 GATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGC 961
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y     1742 CACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGACATGCATTGCCTAC 1801
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y     1802 TCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATTC 1861
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y     1862 CACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGC 1921
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Db    1981 ATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGC 2040

Qy    2042 CGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCCT 2101
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 CGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCCT 2100

Qy    2102 GTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAAT 2161
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 GTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAAT 2160

Qy    2162 GCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTA 2221
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161 GCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTA 2220

Qy    2222 GGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTG 2281
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221 GGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTG 2280

Qy    2282 AAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAA 2341
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 AAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAA 2340

Qy    2342 GTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGACCAGCAACACCGTG 2401
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 GTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGACCAGCAACACCGTG 2400

Qy    2402 ACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATC 2461
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401 ACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATC 2460

Qy    2462 ACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGG 2521
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461 ACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGG 2520

Qy    2522 GTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACA 2581
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2521 GTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACA 2580

Qy    2582 GCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTAT 2641
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581 GCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTAT 2640

Qy    2642 CAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCCT 2701
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641 CAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCCT 2700

Qy    2702 GATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGG 2761
           |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2701 GATGCCCCACCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGG 2760

Qy    2762 AGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGT 2821
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761 AGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGT 2820

Qy    2822 AGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAA 2881
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821 AGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAA 2880

Qy    2882 CCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCT 2941
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881 CCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCT 2940

Qy    2942 GTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGG 3001
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941 GTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGG 3000

Qy    3002 GACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAG 3061
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001 GACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAG 3060
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Qy        3062 AGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGG 3121
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3061 AGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGG 3120

Qy        3122 CAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTC 3181
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3121 CAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTC 3180

Qy        3182 ACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCT 3241
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3181 ACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCT 3240

Qy        3242 CAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCT 3301
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3241 CAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCT 3300

Qy        3302 ACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGTG 3361
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3301 ACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGTG 3360

Qy        3362 GGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTAC 3421
               ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        3361 GGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGACTCCAAGTAC 3420

Qy        3422 CCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGC 3481
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3421 CCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGC 3480

Qy        3482 AACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATT 3541
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3481 AACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATT 3540

Qy        3542 CCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCCA 3601
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3541 CCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCCA 3600

Qy        3602 AGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTG 3661
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3601 AGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTG 3660

Qy        3662 ACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTAC 3721
               |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db        3661 ACTTCAGACTCAGGAAACATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTAC 3720

Qy        3722 ACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTG 3781
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3721 ACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTG 3780

Qy        3782 ACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTC 3841
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3781 ACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTC 3840

Qy        3842 ACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACC 3901
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3841 ACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACC 3900

Qy        3902 CCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCC 3961
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3901 CCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCC 3960

Qy        3962 TGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAG 4021
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3961 TGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAG 4020

Qy        4022 GATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCACT 4081
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4021 GATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCACT 4080

Qy        4082 GACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCCA 4141
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4081 GACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCCA 4140

Qy        4142 TCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGTT 4201
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4141 TCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGTT 4200

Qy        4202 GCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGGT 4261
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4201 GCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGGT 4260

Qy        4262 ACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGA 4321
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4261 ACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGA 4320

Qy        4322 GGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGCC 4381
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4321 GGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGCC 4380

Qy        4382 AACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGC 4441
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4381 AACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGC 4440

Qy        4442 CATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAAT 4501
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4441 CATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAAT 4500

Qy        4502 TCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCTT 4561
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4501 TCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCTT 4560

Qy        4562 AATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCG 4621
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4561 AATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCG 4620

Qy        4622 AGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCCT 4681
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4621 AGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCCT 4680

Qy        4682 GCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGTC 4741
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4681 GCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGTC 4740

Qy        4742 CAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGGA 4801
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4741 CAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGGA 4800

Qy        4802 GTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGC 4861
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4801 GTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGC 4860

Qy        4862 AAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACC 4921
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4861 AAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACC 4920

Qy        4922 GATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGT 4981
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4921 GATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGT 4980

Qy        4982 TACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGGT 5041
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4981 TACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGGT 5040

Qy        5042 CCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAGT 5101
               ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        5041 CCAGATCAAACAGAAATGACTATTGAAAGCTTGCAGCCCACAGTGGAGTATGTGGTTAGT 5100

Qy        5102 GTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAAC 5161
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5101 GTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAAC 5160

Qy        5162 ATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGCT 5221
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5161 ATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGCT 5220

Qy        5222 TGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGAT 5281
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b          5221 TGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGAT 5280

)y          5282 GGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGC 5341
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b          5281 GGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGC 5340

)y          5342 CTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAGC 5401
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b          5341 CTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAGC 5400

)y          5402 CAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCACT 5461
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b          5401 CAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCACT 5460

)y          5462 CAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGGA 5521
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b          5461 CAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGGA 5520

)y          5522 TATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCT 5581
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b          5521 TATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCT 5580

)y          5582 CCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAGT 5641
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b          5581 CCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAGT 5640

)y          5642 GTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTGTCACCACTCTG 5701
                 |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
)b          5641 GTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGTTGTCACCACTCTG 5700

)y          5702 GAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACC 5761
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b          5701 GAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACC 5760

)y          5762 ATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGATGCCGTTCCAGCC 5821
                 |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
)b          5761 ATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCC 5820

)y          5822 AATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACT 5881
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b          5821 AATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACA 5880

)y          5882 GGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGG 5941
                 || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b          5881 GGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGG 5940

)y          5942 AGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTC 6001
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b          5941 AGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTC 6000

)y          6002 CTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACC 6061
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b          6001 CTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACC 6060

)y          6062 GGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCC 6121
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b          6061 GGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCC 6120

)y          6122 CGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATT 6181
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b          6121 CGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATT 6180

)y          6182 TATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACA 6241
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b          6181 TATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACA 6240

)y          6242 GACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTTG 6301
                 | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b          6241 GGCGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTTG 6300

)y          6302 GATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGGA 6361
                 |||||||||||||||||||||||||||||||||| |||||||||| ||||||||||||||
)b          6301 GATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGCCACCCACCCTAGGTATGACACTGGA 6360

Qy          6362 AATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGATC 6421
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6361 AATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGATC 6420

Qy          6422 TTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCAT 6481
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6421 TTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCAT 6480

Qy          6482 AGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTCA 6541
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6481 AGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTCA 6540

Qy          6542 TGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTGTTGGCACTGAT 6601
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6541 TGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTGTTGGCACTGAT 6600

Qy          6602 GAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTCTGACAGGCCTC 6661
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6601 GAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTCTGACAGGCCTC 6660

Qy          6662 ACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAAG 6721
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6661 ACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAAG 6720

Qy          6722 GTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACG 6781
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Qy          6842 CGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCAT 6901
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Qy          7322 GATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCTCTCTGCCAAGA 7381
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RESULT 4
HSM806171
LOCUS       HSM806171               8035 bp    mRNA    linear   PRI 17-JUN-2003
DEFINITION  Homo sapiens mRNA; cDNA DKFZp686E169 (from clone DKFZp686E169).
ACCESSION   BX538018
VERSION     BX538018.1  GI:31874110
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8035)
  AUTHORS   Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by EMBL (European Molecular Biology Laboratories,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp686E169) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             99.6%;  Score 7760.4;  DB 9;  Length 8035;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 7773;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          2 GGCTCGAGCCGGCTGTGCTGCACAGGGGGAGGAGAGGGAACCCCAGGCGCGAGCGGGAAG 61
              ||| || |||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db          1 GGCCCGCGCCGGCTGTGCTGCACAGGGGGAGGAGAGGGAACCCCAGGTGCGAGCGGGAAG 60

Qy         62 AGGGGACCTGCAGCCACAACTTCTCTGGTCCTCTGCATCCCTTCTGTCCCTCCACCCGTC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        122 CCCTTCCCCACCCTCTGGCCCCCACCTTCTTGGAGGCGACAACCCCCGGGAGGCATTAGA 181
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y       302 CTGGCCGTCCTGTGCCTGGGGACAGCGGTGCCCTCCACGGGAGCCTCGAAGAGCAAGAGG 361
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y       362 CAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCGGT 421
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y       422 TGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGC 481
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y       482 AATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAACCT 541
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b       481 AATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAGAGTAAACCT 540

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y       602 TATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGG 661
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Qy     1802 TCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATTC 1861
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Qy     1862 CACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGC 1921
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Qy     1922 AGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCAA 1981
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Qy     2042 CGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCCT 2101
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Qy     2102 GTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAAT 2161
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Qy     2162 GCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTA 2221
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2161 GCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTA 2220

Qy     2222 GGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTG 2281
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2221 GGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTG 2280

Qy     2282 AAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAA 2341
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2281 AAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAA 2340

Qy     2342 GTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGACCAGCAACACCGTG 2401
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2341 GTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGACCAGCAACACCGTG 2400

Qy     2402 ACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATC 2461
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2401 ACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATC 2460

Qy     2462 ACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGG 2521
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2461 ACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGG 2520

Qy        2522 GTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACA 2581
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2521 GTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACA 2580

Qy        2582 GCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTAT 2641
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2581 GCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTAT 2640

Qy        2642 CAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCCT 2701
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2641 CAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCCT 2700

Qy        2702 GATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGG 2761
               |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2701 GATGCCCCACCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGG 2760

Qy        2762 AGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGT 2821
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2761 AGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGT 2820

Qy        2822 AGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAA 2881
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2821 AGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAA 2880

Qy        2882 CCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCT 2941
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2881 CCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCT 2940

Qy        2942 GTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGG 3001
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2941 GTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGG 3000

Qy        3002 GACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAG 3061
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3001 GACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAG 3060

Qy        3062 AGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGG 3121
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3061 AGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGG 3120

Qy        3122 CAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTC 3181
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3121 CAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTC 3180

Qy        3182 ACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCT 3241
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3181 ACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCT 3240

Qy        3242 CAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCT 3301
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3241 CAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCT 3300

Qy        3302 ACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGTG 3361
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3301 ACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGTG 3360

Qy        3362 GGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTAC 3421
               ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        3361 GGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGACTCCAAGTAC 3420

Qy        3422 CCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGC 3481
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3421 CCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGC 3480

Qy        3482 AACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATT 3541
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3481 AACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATT 3540

Qy        3542 CCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCCA 3601
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3541 CCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCCA 3600

Qy        3602 AGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTG 3661
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3601 AGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTG 3660

Qy        3662 ACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTAC 3721
               |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db        3661 ACTTCAGACTCAGGAAACATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTAC 3720

Qy        3722 ACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTG 3781
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3721 ACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTG 3780

Qy        3782 ACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTC 3841
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3781 ACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTC 3840

Qy        3842 ACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACC 3901
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3841 ACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACC 3900

Qy        3902 CCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCC 3961
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3901 CCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCC 3960

Qy        3962 TGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAG 4021
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3961 TGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAG 4020

Qy        4022 GATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCACT 4081
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4021 GATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCACT 4080

Qy        4082 GACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCCA 4141
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4081 GACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCCA 4140

Qy        4142 TCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGTT 4201
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4141 TCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGTT 4200

Qy        4202 GCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGGT 4261
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4201 GCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGGT 4260

Qy        4262 ACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGA 4321
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4261 ACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGA 4320

Qy        4322 GGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGCC 4381
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4321 GGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGCC 4380

Qy        4382 AACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGC 4441
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4381 AACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGC 4440

Qy        4442 CATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAAT 4501
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4441 CATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAAT 4500

Qy        4502 TCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCTT 4561
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4501 TCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCTT 4560

Qy        4562 AATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCG 4621
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4561 AATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCG 4620

Qy        4622 AGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCCT 4681
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4621 AGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCCT 4680
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y         4682 GCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGTC 4741
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         4681 GCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGTC 4740

y         4742 CAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGGA 4801
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         4741 CAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGGA 4800

y         4802 GTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGC 4861
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         4801 GTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGC 4860

y         4862 AAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACC 4921
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         4861 AAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACC 4920

y         4922 GATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGT 4981
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         4921 GATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGT 4980

y         4982 TACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGGT 5041
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         4981 TACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGGT 5040

y         5042 CCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAGT 5101
               ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
b         5041 CCAGATCAAACAGAAATGACTATTGAAAGCTTGCAGCCCACAGTGGAGTATGTGGTTAGT 5100

y         5102 GTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAAC 5161
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         5101 GTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAAC 5160

y         5162 ATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGCT 5221
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         5161 ATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGCT 5220

y         5222 TGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGAT 5281
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         5221 TGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGAT 5280

y         5282 GGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGC 5341
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         5281 GGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGC 5340

y         5342 CTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAGC 5401
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         5341 CTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAGC 5400

y         5402 CAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCACT 5461
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         5401 CAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCACT 5460

y         5462 CAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGGA 5521
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         5461 CAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGGA 5520

y         5522 TATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCT 5581
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         5521 TATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCT 5580

y         5582 CCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAGT 5641
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         5581 CCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAGT 5640

y         5642 GTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTGTCACCACTCTG 5701
               |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
b         5641 GTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGTTGTCACCACTCTG 5700

y         5702 GAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACC 5761
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         5701 GAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACC 5760

y         5762 ATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGATGCCGTTCCAGCC 5821

               |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        5761 ATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCC 5820

Qy        5822 AATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACT 5881
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db        5821 AATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACA 5880

Qy        5882 GGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGG 5941
               || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5881 GGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGG 5940

Qy        5942 AGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTC 6001
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5941 AGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTC 6000

Qy        6002 CTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACC 6061
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6001 CTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACC 6060

Qy        6062 GGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCC 6121
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6061 GGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCC 6120

Qy        6122 CGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATT 6181
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6121 CGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATT 6180

Qy        6182 TATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACA 6241
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6181 TATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACA 6240

Qy        6242 GACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTTG 6301
               | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6241 GGCGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTTG 6300

Qy        6302 GATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGGA 6361
               |||||||||||||||||||||||||||||||||| |||||||||| ||||||||||||||
Db        6301 GATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGCCACCCACCCTAGGTATGACACTGGA 6360

Qy        6362 AATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGATC 6421
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6361 AATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGATC 6420

Qy        6422 TTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCAT 6481
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6421 TTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCAT 6480

Qy        6482 AGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTCA 6541
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6481 AGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTCA 6540

Qy        6542 TGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTGTTGGCACTGAT 6601
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6541 TGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTGTTGGCACTGAT 6600

Qy        6602 GAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTCTGACAGGCCTC 6661
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6601 GAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTCTGACAGGCCTC 6660

Qy        6662 ACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAAG 6721
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6661 ACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAAG 6720

Qy        6722 GTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACG 6781
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6721 GTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACG 6780

Qy        6782 GATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGGAGATGAGTGGGAA 6841
               ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        6781 GATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGGAGATGAGTGGGAA 6840

Qy        6842 CGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCAT 6901
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         6902 TTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGAG 6961
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Qy         6962 AAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTCTTGGGAACGGA 7021
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Qy         7022 AAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGATGGGAAGACATAC 7081
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Qy         7082 CACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTTT 7141
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Qy         7142 GGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGGTGAACCCAGTCCC 7201
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Qy         7202 GAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCATCAGAGAACAAAC 7261
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Qy         7262 ACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGGCTGACAGAGAA 7321
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Qy         7322 GATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCTCTCTGCCAAGA 7381
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Qy         7382 TCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTCTTTCTTTCTTAAG 7441
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Qy         7442 CCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCTTCTCCAAGCATCA 7501
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Qy         7682 TTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGTCTGGCCCGCAATA 7741
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Qy         7742 CTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCACAGTACT 7795
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RESULT 5
HSM806901
LOCUS       HSM806901                7951 bp    mRNA    linear   PRI 28-AUG-2003
DEFINITION  Homo sapiens mRNA; cDNA DKFZp686F219 (from clone DKFZp686F219);
            complete cds.
ACCESSION   BX640802
VERSION     BX640802.1  GI:34364927
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 7951)
  AUTHORS   Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  CONSRTM   The German Human cDNA Consortium
  TITLE     Direct Submission
  JOURNAL   Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by EMBL (European Molecular Biology Laboratories,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp686F219) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.
FEATURES             Location/Qualifiers
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                     IPVNLPGEHGQRLPISRNTFAEVTGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKLDA
                     PTNLQLSMKLILLSW"
ORIGIN

  Query Match             97.0%;  Score 7562.4;  DB 9;  Length 7951;
  Best Local Similarity   98.7%;  Pred. No. 0;
  Matches 7694;  Conservative    0;  Mismatches   21;  Indels   79;  Gaps    4;

Qy            2 GGCTCGAGCCGGCTGTGCTGCACAGGGGGAGGAGAGGGAACCCCAGGCGCGAGCGGGAAG 61
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Qy           62 AGGGGACCTGCAGCCACAACTTCTCTGGTCCTCTGCATCCCTTCTGTCCCTCCACCCGTC 121
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Qy        122 CCCTTCCCCACCCTCTGGCCCCCACCTTCTTGGAGGCGACAACCCCCGGGAGGCATTAGA 181
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Db        123 CCCTTCCCCACCCTCTGGCCCCCACCTTCTTGGAGGCGACAACCCCCGGGAGGCATTAGA 182

Qy        182 AGGGATTTTTCCCGCAGGTTGCGAAGGGAAGCAAACTTGGTGGCAACTTGCCTCCCGGTG 241
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Qy        242 CGGGCGTCTCTCCCCCACCGTCTCAACATGCTTAGGGGTCCGGGGCCCGGGCTGCTGCTG 301
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Qy        422 TGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGC 481
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Qy        482 AATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAACCT 541
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Qy        542 GAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACACT 601
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Qy        602 TATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGG 661
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Db        603 TATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGG 662

Qy        662 AGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGGT 721
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Db        663 AGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGGT 722

Qy        722 GACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTGTGTGTGTCTTGGT 781
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Qy        782 AATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGCT 841
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Qy        842 GGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGTA 901
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Qy        902 GATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGC 961
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Qy        962 AACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAAT 1021
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Qy       1022 CGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAG 1081
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Qy       1202 AGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGGAAATAAGCAAATG 1261
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Qy       1622 TATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGAGGAAATCTGCACA 1681
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Qy       1802 TCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATTC 1861
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Qy       1862 CACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGC 1921
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Qy       1922 AGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCAA 1981
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Qy       2222 GGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTG 2281
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Qy       2282 AAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAA 2341
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Qy        2342 GTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGACCAGCAACACCGTG 2401
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Qy        2462 ACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGG 2521
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2463 ACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGG 2522

Qy        2522 GTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACA 2581
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Db        2523 GTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACA 2582

Qy        2582 GCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTAT 2641
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Qy        2642 CAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCCT 2701
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Qy        2702 GATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGG 2761
               |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        2762 AGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGT 2821
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2763 AGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGT 2822

Qy        2822 AGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAA 2881
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2823 AGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAA 2882

Qy        2882 CCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCT 2941
               ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        2883 CCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAGGTACACCT 2942

Qy        2942 GTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGG 3001
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2943 GTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGG 3002

Qy        3002 GACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAG 3061
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3003 GACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAG 3062

Qy        3062 AGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGG 3121
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3063 AGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGG 3122

Qy        3122 CAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTC 3181
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3123 CAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTC 3182

Qy        3182 ACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCT 3241
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3183 ACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCT 3242

Qy        3242 CAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCT 3301
               ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        3243 CAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAG-TTGTCAATGAAACTGATTCT 3301

Qy        3302 ACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGTG 3361
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3302 ACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGTG 3361

Qy        3362 GGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTAC 3421
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3362 GGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTAC 3421

Qy        3422 CCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGC 3481
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3422 CCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGC 3481

Qy        3482 AACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATT 3541
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3482 AACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATT 3541

Qy        3542 CCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCCA 3601
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3542 CCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCCA 3601

Qy        3602 AGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTG 3661
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3602 AGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTG 3661

Qy        3662 ACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTAC 3721
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3662 ACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTAC 3721

Qy        3722 ACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTG 3781
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3722 ACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTG 3781

Qy        3782 ACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTC 3841
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3782 ACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTC 3841

Qy        3842 ACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACC 3901
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3842 ACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACC 3901

Qy        3902 CCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCC 3961
               |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db        3902 CCTACAAACGGCCAGCGGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCC 3961

Qy        3962 TGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAG 4021
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        3962 TGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGCCAAG 4021

Qy        4022 GATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCACT 4081
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4022 GATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCACT 4081

Qy        4082 GACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCCA 4141
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4082 GACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCCA 4141

Qy        4142 TCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGTT 4201
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4142 TCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGTT 4201

Qy        4202 GCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGGT 4261
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4202 GCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGGT 4261

Qy        4262 ACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGA 4321
               ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        4262 ACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACACCATGAGAGCACACCTCTTAGA 4321

Qy        4322 GGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGCC 4381
               ||||||||| |||||||||||||||||||||||||||||||||||        |||||||
Db        4322 GGAAGACAG-AAACAGGTCTTGATTCCCCAACTGGCATTGACTTT--CTGATATACTGCC 4378

Qy        4382 AACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGC 4441
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4379 AACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGC 4438

Qy        4442 CATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAAT 4501
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4439 CATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAAT 4498
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y      4502 TCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCTT 4561
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      4499 TCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCTT 4558

y      4562 AATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCG 4621
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      4559 AATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCG 4618

y      4622 AGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCCT 4681
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      4619 AGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCCT 4678

y      4682 GCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGTC 4741
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      4679 GCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGTC 4738

y      4742 CAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGGA 4801
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      4739 CAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGGA 4798

y      4802 GTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGC 4861
            |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
b      4799 GTTGATTATACCATCAATGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGC 4858

y      4862 AAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACC 4921
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      4859 AAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACC 4918

y      4922 GATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGT 4981
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      4919 GATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGT 4978

y      4982 TACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGGT 5041
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      4979 TACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGGT 5038

y      5042 CCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAGT 5101
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      5039 CCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAGT 5098

y      5102 GTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAAC 5161
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      5099 GTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAAC 5158

y      5162 ATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGCT 5221
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      5159 ATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGCT 5218

y      5222 TGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGAT 5281
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      5219 TGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGAT 5278

y      5282 GGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGC 5341
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      5279 GGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGC 5338

y      5342 CTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAGC 5401
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      5339 CTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAGC 5398

y      5402 CAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCACT 5461
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      5399 CAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCACT 5458

y      5462 CAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGGA 5521
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      5459 CAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGGA 5518

y      5522 TATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCT 5581
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      5519 TATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCT 5578

Qy     5582 CCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAGT 5641
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5579 CCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAGT 5638

Qy     5642 GTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTGTCACCACTCTG 5701
            |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db     5639 GTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGTTGTCACCACTCTG 5698

Qy     5702 GAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACC 5761
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5699 GAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACC 5758

Qy     5762 ATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGATGCCGTTCCAGCC 5821
            |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db     5759 ATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCC 5818

Qy     5822 AATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACT 5881
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db     5819 AATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACA 5878

Qy     5882 GGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGG 5941
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5879 GGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGG 5938

Qy     5942 AGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTC 6001
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5939 AGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTC 5998

Qy     6002 CTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACC 6061
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5999 CTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACC 6058

Qy     6062 GGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCC 6121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6059 GGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCC 6118

Qy     6122 CGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATT 6181
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6119 CGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATT 6178

Qy     6182 TATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACA 6241
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6179 TATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAG--- 6235

Qy     6242 GACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTTG 6301

Db     6236 ------------------------------------------------------------ 6235

Qy     6302 GATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGGA 6361
                        ||||||||||||||||||||||||||||||||||||||||||||||||
Db     6236 ------------ACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGGA 6283

Qy     6362 AATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGATC 6421
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6284 AATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGATC 6343

Qy     6422 TTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCAT 6481
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6344 TTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCAT 6403

Qy     6482 AGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTCA 6541
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6404 AGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTCA 6463

Qy     6542 TGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTGTTGGCACTGAT 6601
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6464 TGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTGTTGGCACTGAT 6523

Qy     6602 GAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTCTGACAGGCCTC 6661
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6524 GAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTCTGACAGGCCTC 6583

Qy     6662 ACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAAG 6721
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6584 ACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAAG 6643.

Qy       6722 GTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACG 6781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6644 GTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACG 6703

Qy       6782 GATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGGAGATGAGTGGGAA 6841
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       6704 GATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGGAGATGAGTGGGAA 6763

Qy       6842 CGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCAT 6901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6764 CGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCAT 6823

Qy       6902 TTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGAG 6961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6824 TTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGAG 6883

Qy       6962 AAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTCTTGGGAACGGA 7021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6884 AAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTCTTGGGAACGGA 6943

Qy       7022 AAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGATGGGAAGACATAC 7081
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       6944 AAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTATGATGATGGGAAGACATAC 7003

Qy       7082 CACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTTT 7141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7004 CACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTTT 7063

Qy       7142 GGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGGTGAACCCAGTCCC 7201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7064 GGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGGTGAACCCAGTCCC 7123

Qy       7202 GAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCATCAGAGAACAAAC 7261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7124 GAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCATCAGAGAACAAAC 7183

Qy       7262 ACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGGCTGACAGAGAA 7321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7184 ACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGGCTGACAGAGAA 7243

Qy       7322 GATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCTCTCTGCCAAGA 7381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7244 GATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCTCTCTGCCAAGA 7303

Qy       7382 TCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTCTTTCTTTCTTAAG 7441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7304 TCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTCTTTCTTTCTTAAG 7363

Qy       7442 CCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCTTCTCCAAGCATCA 7501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7364 CCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCTTCTCCAAGCATCA 7423

Qy       7502 CCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATTGCCTGTTCTGCTT 7561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7424 CCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATTGCCTGTTCTGCTT 7483

Qy       7562 CGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATTTGGTTTGGGAT 7621
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RESULT 6
HSM806902
LOCUS       HSM806902               7951 bp    mRNA    linear   PRI 30-AUG-2003
DEFINITION  Homo sapiens mRNA; cDNA DKFZp686K139 (from clone DKFZp686K139);
            complete cds.
ACCESSION   BX649182
VERSION     BX649182.1  GI:34366424
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 7951)
  AUTHORS   Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  CONSRTM   The German Human cDNA Consortium
  TITLE     Direct Submission
  JOURNAL   Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by EMBL (European Molecular Biology Laboratories,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp686K139) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.
FEATURES             Location/Qualifiers
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)RIGIN

 Query Match              97.0%;  Score 7562.4;  DB 9;  Length 7951;
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 Matches 7694;  Conservative    0;  Mismatches   21;  Indels   79;  Gaps    4;

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)y        542 GAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACACT 601
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)y        662 AGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGGT 721
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)y        902 GATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGC 961
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Qy       1022 CGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAG 1081
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Qy       1202 AGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGGAAATAAGCAAATG 1261
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Qy       1562 ACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGGGACCACACAGAAC 1621
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Qy       1622 TATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGAGGAAATCTGCACA 1681
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Qy       1802 TCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATTC 1861
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Qy       1922 AGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCAA 1981
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Qy       2162 GCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTA 2221
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Qy       2282 AAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAA 2341
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Qy       2402 ACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATC 2461
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Db       2403 ACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATC 2462

Qy       2462 ACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGG 2521
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2463 ACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGG 2522

Qy       2522 GTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACA 2581
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2523 GTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACA 2582

Qy       2582 GCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTAT 2641
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2583 GCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTAT 2642

Qy       2642 CAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCCT 2701
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Qy       2702 GATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGG 2761
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2703 GATGCCCCACCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGG 2762

Qy       2762 AGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGT 2821
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2822 AGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAA 2881
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2882 CCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCT 2941
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Db       2883 CCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAGGTACACCT 2942

Qy       2942 GTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGG 3001
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Qy       3002 GACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAG 3061
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Qy       3122 CAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTC 3181
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Qy       3182 ACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCT 3241
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Qy       3242 CAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCT 3301
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Db       3243 CAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAG-TTGTCAATGAAACTGATTCT 3301

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Qy       3362 GGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTAC 3421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3362 GGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTAC 3421

Qy       3422 CCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGC 3481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3422 CCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGC 3481

Qy       3482 AACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATT 3541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3482 AACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATT 3541

Qy       3542 CCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCCA 3601
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Qy       3602 AGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTG 3661
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Qy       3662 ACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTAC 3721
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Db       3662 ACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTAC 3721

Qy       3722 ACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTG 3781
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Qy       3782 ACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTC 3841
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Qy       3842 ACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACC 3901
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Qy       3902 CCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCC 3961
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Qy       3962 TGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAG 4021
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Qy       4022 GATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCACT 4081
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Qy       4082 GACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCCA 4141
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Qy       4142 TCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGTT 4201
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Qy       4202 GCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGGT 4261
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Qy       4262 ACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGA 4321
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b         4262 ACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACACCATGAGAGCACACCTCTTAGA 4321

y         4322 GGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGCC 4381
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b         4322 GGAAGACAG-AAACAGGTCTTGATTCCCCAACTGGCATTGACTTT--CTGATATACTGCC 4378

y         4382 AACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGC 4441
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         4379 AACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGC 4438

y         4442 CATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAAT 4501
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y         4502 TCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCTT 4561
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y         4562 AATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCG 4621
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b         4559 AATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCG 4618

y         4622 AGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCCT 4681
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y         4682 GCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGTC 4741
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y         4742 CAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGGA 4801
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y         4802 GTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGC 4861
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y         4922 GATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGT 4981
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         4919 GATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGT 4978

y         4982 TACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGGT 5041
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b         4979 TACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGGT 5038

y         5042 CCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAGT 5101
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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y         5102 GTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAAC 5161
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b         5099 GTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAAC 5158

y         5162 ATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGCT 5221
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b         5159 ATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGCT 5218

y         5222 TGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGAT 5281
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b         5219 TGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGAT 5278

y         5282 GGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGC 5341
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         5279 GGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGC 5338

y         5342 CTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAGC 5401
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         5339 CTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAGC 5398
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Qy        5402 CAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCACT 5461
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Db        5399 CAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCACT 5458

Qy        5462 CAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGGA 5521
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Qy        5522 TATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCT 5581
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Qy        5582 CCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAGT 5641
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Qy        5642 GTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTGTCACCACTCTG 5701
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Qy        5762 ATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGATGCCGTTCCAGCC 5821
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Db        5759 ATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCC 5818

Qy        5822 AATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACT 5881
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Qy        5882 GGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGG 5941
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Qy        5942 AGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTC 6001
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Qy        6062 GGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCC 6121
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Qy        6122 CGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATT 6181
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Qy        6182 TATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACA 6241
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Qy        6242 GACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTTG 6301

Db        6236 ------------------------------------------------------------ 6235

Qy        6302 GATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGGA 6361
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Db        6236 ------------ACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGGA 6283

Qy        6362 AATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGATC 6421
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Qy        6422 TTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCAT 6481
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Qy       6482 AGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTCA 6541
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Qy       6662 ACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAAG 6721
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Qy       6842 CGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCAT 6901
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Qy       7322 GATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCTCTCTGCCAAGA 7381
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RESULT 7
HSM806267
LOCUS       HSM806267               8320 bp    mRNA    linear   PRI 17-JUN-2003
DEFINITION  Homo sapiens mRNA; cDNA DKFZp686I155 (from clone DKFZp686I155).
ACCESSION   BX537590
VERSION     BX537590.1  GI:31873669
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8320)
  AUTHORS   Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by GBF (National Research Centre for Biotechnology Ltd.,
            Braunschweig/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp686I155) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.
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                     The frame shift was determined manually"
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)b      3721 ACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTG 3780

)y      3782 ACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTC 3841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b      3781 ACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTC 3840

)y      3842 ACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACC 3901
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b      3841 ACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACC 3900

)y      3902 CCTACAAACGGCCAGCAGGGAAATTCTTT-GGAAGAAGTGGTCCATGCTGATCAGAGCTC 3960
             ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
)b      3901 CCTACAAACGGCCAGCAGGGAAATTCTTTGGGAAGAAGTGGTCCATGCTGATCAGAGCTC 3960

)y      3961 CTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAA 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b      3961 CTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAA 4020

)y      4021 GGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCA----------------- 4063
             |||||||||||||||||||||||||||||||||||||||||||
)b      4021 GGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGAGGTGCCCCAACTCAC 4080

)y      4064 ------------------------------------------------------------ 4063

)b      4081 TGACCTAAGCTTTGTTGATATAACCGATTCAAGCATCGGCCTGAGGTGGACCCCGCTAAA 4140

)y      4064 ------------------------------------------------------------ 4063

)b      4141 CTCTTCCACCATTATTGGGTACCGCATCACAGTAGTTGCGGCAGGAGAAGGTATCCCTAT 4200

)y      4064 ------------------------------------------------------------ 4063

)b      4201 TTTTGAAGATTTTGTGGACTCCTCAGTAGGATACTACACAGTCACAGGGCTGGAGCCGGG 4260

)y      4064 ------------------------------------------------------------ 4063

)b      4261 CATTGACTATGATATCAGCGTTATCACTCTCATTAATGGCGGCGAGAGTGCCCCTACTAC 4320

)y      4064 ----------------GCTGTTCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCC 4107
                             ||||||||||||||||||||||||||||||||||||||||||||
)b      4321 ACTGACACAACAAACGGCTGTTCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCC 4380

)y      4108 AGACACCATGCGTGTCACCTGGGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGT 4167
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b      4381 AGACACCATGCGTGTCACCTGGGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGT 4440

)y      4168 GCGTTACTCACCTGTGAAAAATGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGA 4227
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b      4441 GCGTTACTCACCTGTGAAAAATGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGA 4500

)y      4228 CAATGCAGTGGTCTTAACAAATCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAG 4287
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)b      4501 CAATGCAGTGGTCTTAACAAATCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAG 4560

)y      4288 TGTCTACGAACAACATGAGAGCACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTC 4347
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)y      4348 CCCAACTGGCATTGACTTTTCTGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGC 4407
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)y      4408 TCCTCGAGCCACCATCACTGGCTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAG 4467
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)y      4468 ACCTCGAGAAGATCGGGTGCCCCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCC 4527
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)b      4741 ACCTCGAGAAGATCGGGTGCCCCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCC 4800

)y      4528 AGGCACAGAGTATGTGGTCAGCATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATT 4587
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)b      4801 AGGCACAGAGTATGTGGTCAGCATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATT 4860
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Qy      4588 GATTGGCCAACAATCAACAGTTTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGAC 4647
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Db      4861 GATTGGCCAACAATCAACAGTTTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGAC 4920

Qy      4648 CCCCACCAGCCTACTGATCAGCTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGAT 4707
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4921 CCCCACCAGCCTACTGATCAGCTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGAT 4980

Qy      4708 CACTTACGGAGAAACAGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAA 4767
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4981 CACTTACGGAGAAACAGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAA 5040

Qy      4768 GTCTACAGCTACCATCAGCGGCCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGC 4827
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Db      5041 GTCTACAGCTACCATCAGCGGCCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGC 5100

Qy      4828 TGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAAC 4887
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Db      5101 TGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAAC 5160

Qy      4888 AGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGT 4947
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Qy      4948 CAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAA 5007
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Db      5221 CAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAA 5280

Qy      5008 TGGACCAGGACCAACAAAAACTAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGA 5067
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      5068 AGGCTTGCAGCCCACAGTGGAGTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGA 5127
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Db      5341 AGGCTTGCAGCCCACAGTGGAGTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGA 5400

Qy      5128 GAGTCAGCCTCTGGTTCAGACTGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATT 5187
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Db      5401 GAGTCAGCCTCTGGTTCAGACTGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATT 5460

Qy      5188 CACTGATGTGGATGTCGATTCCATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTC 5247
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Db      5461 CACTGATGTGGATGTCGATTCCATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTC 5520

Qy      5248 CAGGTACAGGGTGACCTACTCGAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACC 5307
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5521 CAGGTACAGGGTGACCTACTCGAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACC 5580

Qy      5308 TGATGGTGAAGAAGACACTGCAGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGT 5367
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5581 TGATGGTGAAGAAGACACTGCAGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGT 5640

Qy      5368 CAGTGTGGTTGCCTTGCACGATGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCAC 5427
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Db      5641 CAGTGTGGTTGCCTTGCACGATGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCAC 5700

Qy      5428 AGCTATTCCTGCACCAACTGACCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGC 5487
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5701 AGCTATTCCTGCACCAACTGACCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGC 5760

Qy      5488 CCAGTGGACACCACCCAATGTTCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGA 5547
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Db      5761 CCAGTGGACACCACCCAATGTTCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGA 5820

Qy      5548 GAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATC 5607
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Qy      5608 AGGACTTATGGTGGCCACCAAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGAC 5667
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Db      5881 AGGACTTATGGTGGCCACCAAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGAC 5940
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Qy          5668 AAGCAGACCAGCTCAGGGAGTTGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGC 5727
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Db          5941 AAGCAGACCAGCTCAGGGTGTTGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGC 6000

Qy          5728 TCGTGTGACAGATGCTACTGAGACCACCATCACCATTAGCTGGAGAACCAAGACTGAGAC 5787
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Db          6001 TCGTGTGACAGATGCTACTGAGACCACCATCACCATTAGCTGGAGAACCAAGACTGAGAC 6060

Qy          5788 GATCACTGGCCTCCAAGTTGATGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAAC 5847
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Qy          5848 CATCAAGCCAGATGTCAGAAGCTACACCATCACTGGCTTACAACCAGGCACTGACTACAA 5907
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Db          6121 CATCAAGCCAGATGTCAGAAGCTACACCATCACAGGTTTACAACCAGGCACTGACTACAA 6180

Qy          5908 GATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTC 5967
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Db          6181 GATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTC 6240

Qy          5968 CACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCT 6027
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Db          6241 CACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCT 6300

Qy          6028 GGTATCATGGCAGCCGCCACGTGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCC 6087
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Db          6301 GGTATCATGGCAGCCGCCACGTGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCC 6360

Qy          6088 TGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTAT 6147
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6361 TGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTAT 6420

Qy          6148 TACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAATCA 6207
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Db          6421 TACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAATCA 6480

Qy          6208 GAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCT 6267
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Db          6481 GAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCT 6540

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Db          6541 TCCACACCCCAATCTTCATGGACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGAC 6600

Qy          6328 CCCTTTCGTCACCCACCCTGGGTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTC 6387
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Qy          6388 TGGTCAGCAACCCAGTGTTGGGCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGAC 6447
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Db          6661 TGGTCAGCAACCCAGTGTTGGGCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGAC 6720

Qy          6448 CACACCGCCCACAACGGCCACCCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGT 6507
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Db          6721 CACACCGCCCACAACGGCCACCCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGT 6780

Qy          6508 AGGACAAGAAGCTCTCTCTCAGACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGA 6567
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Qy          6568 GTACATCATTTCATGTCATCCTGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCC 6627
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Qy          6688 AGTGGAGGCACTGAAAGACCAGCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGG 6747
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Db          7321 TGAGGCAACGTGTTATGATGATGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGA 7380

Qy          7108 ATATCTCGGTGCCATTTGCTCCTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGA 7167
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Qy          7168 CAACTGCCGCAGACCTGGGGGTGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAA 7227
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Qy          7288 CTTCATGCCTTTAGATGTACAGGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCC 7347
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Db          7561 CTTCATGCCTTTAGATGTACAGGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCC 7620

Qy          7348 AATCCAGAGGAACAAGCATGTCTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGC 7407
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Qy          7408 AGACCCAGCTTAGAGTTCTTCTTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCA 7467
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Db          7681 AGACCCAGCTTAGAGTTCTTCTTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCA 7740

Qy          7468 GCTTCAGCTCAACTCACAGCTTCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCT 7527
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Qy          7528 CATAAATGAGGGCTGCACATTGCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATT 7587
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Qy          7588 TTAAATGAAGTGATTCTAAGATTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACC 7647
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Qy          7708 CTTCTGCTTTCACTTAAGTGTCTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTA 7767
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RESULT 8
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R274901
OCUS       AR274901                7679 bp    DNA     linear   PAT 10-APR-2003
EFINITION  Sequence 38 from patent US 6506607.
CCESSION   AR274901
ERSION     AR274901.1  GI:29707451
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 7679)
 AUTHORS   Shyjan,A.W.
 TITLE     Methods and compositions for the identification and assessment of
           prostate cancer therapies and the diagnosis of prostate cancer
 JOURNAL   Patent: US 6506607-A 38 14-JAN-2003;
EATURES             Location/Qualifiers
    source          1..7679
                    /organism="unknown"
                    /mol_type="genomic DNA"
RIGIN

 Query Match             95.2%;  Score 7423;  DB 6;  Length 7679;
 Best Local Similarity   99.8%;  Pred. No. 0;
 Matches 7432;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

y          349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b            1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

y          409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGAGCG 468
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGAGCG 120

y          469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
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b          121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

y          529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
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b          181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

y          589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

y          649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

y          709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

y          769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480

y          829 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          481 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 540

y          889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy         949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

Qy        1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy        1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy        1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy        1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG 1248
               |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db         841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGTTGAAGACACAAGG 900

Qy        1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy        1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
               ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy        1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
               ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy        1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy        1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
               ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy        1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy        1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy        1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy        1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy        1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
               |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy        1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy        1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy        1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy        2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy        2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy        2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy   2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy   2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy   2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy   2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy   2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

Qy   2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

Qy   2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy   2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

Qy   2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy   2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
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Db   2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy   2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

Qy   2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

Qy   2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
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Db   2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

Qy   3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
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Db   2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy   3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
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Db   2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy   3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
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Db   2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy   3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy   3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy   3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy   3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
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Db   3061 TGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy   3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
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Db   3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy   3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
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Db   3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy   3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy   3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
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Db   3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy   3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
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Qy   3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
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Db   3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy   3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy   3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600

Qy   3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy   4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
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Db   3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy   4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
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Db   3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy   4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy   4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
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Db   3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020
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y    4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
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b    4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

y    4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
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b    4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

y    4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

y    4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
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b    4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

y    4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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y    4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
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y    4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
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b    4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

y    4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
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b    4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

y    4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
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y    4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

y    4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

y    5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
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y    5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
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y    5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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y    5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
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y    5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

y    5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy   5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy   5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy   5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy   5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy   5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy   5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy   5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
          ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy   5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
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Db   5461 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5520

Qy   5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
          |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db   5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

Qy   5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

Qy   5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy   6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy   6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

Qy   6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

Qy   6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy   6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
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Db   5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy   6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
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Db   6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy   6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
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Db   6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy   6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
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Db   6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

Qy   6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6181 GACAACCATCTCATGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

Qy      6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
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Db      6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300

Qy      6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
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Db      6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360

Qy      6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
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Db      6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

Qy      6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
             |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db      6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

Qy      6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
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Db      6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

Qy      6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
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Qy      6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

Qy      7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6661 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 6720

Qy      7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

Qy      7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6781 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840

Qy      7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6841 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 6900

Qy      7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
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Db      6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960

Qy      7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
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Db      6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

Qy      7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080

Qy      7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
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Db      7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

Qy      7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

Qy      7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260

Qy      7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

Qy      7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy      7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440

Qy      7789 CAGTACT 7795
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Db      7441 CAGTACT 7447


RESULT 9
AR380744
LOCUS       AR380744                7680 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1289 from patent US 6607879.
ACCESSION   AR380744
VERSION     AR380744.1  GI:40088378
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 7680)
  AUTHORS   Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
  TITLE     Compositions for the detection of blood cell and immunological
            response gene expression
  JOURNAL   Patent: US 6607879-A 1289 19-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .7680
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             95.2%;  Score 7423;  DB 6;  Length 7680;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7432;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy       349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy       409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy       469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
             |||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db       121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy       529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

Qy       589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

Qy       649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy       709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy       769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480

Qy       829 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       481 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 540

y       889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

y       949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

y      1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

y      1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

y      1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

y      1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG 1248
            |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
b       841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGTTGAAGACACAAGG 900

y      1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

y      1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
            ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
b       961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

y      1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
            ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
b      1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

y      1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

y      1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
b      1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

y      1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

y      1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

y      1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
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b      1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

y      1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

y      1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
            |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
b      1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

y      1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
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b      1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

y      1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy     1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy     2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy     2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy     2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
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Db     1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy     2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy     2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy     2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy     2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy     2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

Qy     2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

Qy     2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy     2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

Qy     2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy     2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy     2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

Qy     2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

Qy     2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

Qy     2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700
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Qy   3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy   3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy   3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy   3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy   3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy   3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy   3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   3061 TGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy   3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy   3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy   3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy   3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy   3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy   3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy   3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy   3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600

Qy   3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy   4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy   4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy   4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy   4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy   4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy   4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy   4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy   4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy   4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy   4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy   4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4320

Qy   4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy   4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy   4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy   4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy   4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

Qy   4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

Qy   5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy   5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800

Qy   5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy   5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

y        5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

y        5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

y        5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

y        5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

y        5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

y        5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

y        5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
b        5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

y        5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

y        5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
b        5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

y        5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        5461 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5520

y        5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
              |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
b        5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

y        5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

y        5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

y        6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

y        6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

y        6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

y        6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

y        6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000
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Qy       6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy       6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy       6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

Qy       6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6181 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

Qy       6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300

Qy       6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360

Qy       6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

Qy       6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db       6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

Qy       6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

Qy       6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

Qy       6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

Qy       7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6661 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 6720

Qy       7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

Qy       7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
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Qy       7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
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Qy       7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
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Db       6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960

Qy       7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

Qy       7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080
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Qy      7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
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Db      7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

Qy      7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
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Qy      7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
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Qy      7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
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Db      7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

Qy      7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
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Db      7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy      7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440

Qy      7789 CAGTACT 7795
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Db      7441 CAGTACT 7447


RESULT 10
AX277596
LOCUS       AX277596                7680 bp    DNA     linear   PAT 01-NOV-2001
DEFINITION  Sequence 75 from Patent WO0177327.
ACCESSION   AX277596
VERSION     AX277596.1  GI:16604795
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Carulli,J.P., Little,R.D., Recker,R.R. and Johnson,M.L.
  TITLE     The high bone mass gene of 11q13.3
  JOURNAL   Patent: WO 0177327-A 75 18-OCT-2001;
            Genome Therapeutics Corporation (US)
FEATURES             Location/Qualifiers
     source          1..7680
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             95.2%;  Score 7423;  DB 6;  Length 7680;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7432;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy       349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy       409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy       469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
             |||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db       121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy       529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

Qy       589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

Qy       649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy       709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
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Db       361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy       769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
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Db       541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy       949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
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Db       601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

Qy      1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy      1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy      1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy      1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG 1248
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db       841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGTTGAAGACACAAGG 900

Qy      1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy      1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy      1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
             ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db      1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy      1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
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Db      1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy      1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
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Db      1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy      1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy      1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy      1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

y       1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
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b       1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

y       1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
b       1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

y       1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
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b       1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

y       1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
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b       1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

y       1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

y       2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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y       2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
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b       1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

y       2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
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b       1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

y       2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
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b       1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

y       2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

y       2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
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b       1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

y       2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
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b       2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

y       2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
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b       2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

y       2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
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y       2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
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y       2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
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y       2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
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y       2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
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Qy      2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
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Qy      2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
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Qy      2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
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Qy      3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
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Qy      3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
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Db      2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy      3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
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Db      2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy      3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy      3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
             |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db      3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy      3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
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Db      3061 TGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy      3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
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Db      3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy      3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
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Db      3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy      3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
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Db      3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy      3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy      3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
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Db      3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy      3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
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Db      3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy      3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
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Db      3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540
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Qy       3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
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Db       3541 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600

Qy       3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy       4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy       4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy       4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy       4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy       4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy       4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
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Db       4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy       4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy       4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy       4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy       4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
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Db       4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy       4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy       4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
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Db       4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy       4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy       4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
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Db       4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

Qy       5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
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Db       4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy       5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800

Qy       5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy       5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
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Qy       5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
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Qy       5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy       5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
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Db       5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy       5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
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Db       5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy       5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
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Db       5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy       5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
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Db       5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy       5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db       5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy       5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
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Db       5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy       5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
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Db       5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy       5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5461 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5520

Qy       5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
              |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db       5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

Qy       5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
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Qy       5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy       6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy       6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

Qy       6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
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Db       5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

Qy       6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy       6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
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Db       5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy       6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
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Db       6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy       6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
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Db       6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy       6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
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Db       6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

Qy       6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
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Db       6181 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

Qy       6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
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Qy       6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
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Db       6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

Qy       6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
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Db       6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

Qy       6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
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Db       6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

Qy       6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
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Db       6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

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Qy       7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
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Qy       7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
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Qy       7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
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Qy       7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
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Qy       7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
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Qy       7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
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Qy       7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
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Db       7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

Qy       7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
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Db       7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy       7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
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Db       7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440

Qy       7789 CAGTACT 7795
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Db       7441 CAGTACT 7447


RESULT 11
AX335368
LOCUS       AX335368                7680 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 5877 from Patent WO0194629.
ACCESSION   AX335368
VERSION     AX335368.1  GI:18126087
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 5877 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1..7680
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             95.2%;  Score 7423;  DB 6;  Length 7680;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7432;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy      349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy      409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy      469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
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Db      121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy      529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

Qy      589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

Qy      649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy      709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy      769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
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Qy      889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
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Db      541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy      949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
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Db      601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

Qy     1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy     1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy     1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy     1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG 1248
            |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db      841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGTTGAAGACACAAGG 900

Qy     1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy     1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
            ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy     1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
            ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db     1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy     1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy     1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy     1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy     1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy     1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy     1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy     1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
            |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db     1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy     1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy     1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy     1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy     2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy     2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy     2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy     2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy     2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy     2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy     2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy     2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160
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Qy       2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
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Db       2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

Qy       2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy       2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

Qy       2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy       2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy       2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

Qy       2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

Qy       2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

Qy       2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

Qy       3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy       3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
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Db       2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy       3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy       3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy       3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy       3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy       3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
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Qy       3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy       3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
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Db       3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy       3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy       3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy       3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy       3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy       3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy       3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
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Qy       3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
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Qy       4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
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Qy       4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy       4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy       4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy       4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy       4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy       4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
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Qy       4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
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Qy       4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
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Qy       4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
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Qy   4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy   4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
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Qy   4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
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Qy   4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
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Qy   5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
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Qy   5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
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Qy   5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy   5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy   5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
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Qy   5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
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Qy   5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
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Qy   5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
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Qy   5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
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Db   5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy   5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy   5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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ESULT 12
SFIB1
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ERSION     X02761.1  GI:31396
EYWORDS    alternate splicing; fibronectin.
OURCE      Homo sapiens (human)
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REFERENCE   1  (bases 1 to 7680)
  AUTHORS   Kornblihtt,A.R., Vibe-Pedersen,K. and Baralle,F.E.
  TITLE     Isolation and characterization of cDNA clones for human and bovine
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 80 (11), 3218-3222 (1983)
  MEDLINE   83221567
   PUBMED   6304699
REFERENCE   2  (bases 1 to 7680)
  AUTHORS   Kornblihtt,A.R., Vibe-Pedersen,K. and Baralle,F.E.
  TITLE     Human fibronectin: molecular cloning evidence for two mRNA species
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  JOURNAL   EMBO J. 3 (1), 221-226 (1984)
  MEDLINE   84158533
   PUBMED   6200322
REFERENCE   3  (bases 1 to 7680)
  AUTHORS   Kornblihtt,A.R., Vibe-Pedersen,K. and Baralle,F.E.
  TITLE     Human fibronectin: cell specific alternative mRNA splicing
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            repeats
  JOURNAL   Nucleic Acids Res. 12 (14), 5853-5868 (1984)
  MEDLINE   84272258
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REFERENCE   4  (bases 1 to 7680)
  AUTHORS   Kornblihtt,A.R., Umezawa,K., Vibe-Pedersen,K. and Baralle,F.E.
  TITLE     Primary structure of human fibronectin: differential splicing may
            generate at least 10 polypeptides from a single gene
  JOURNAL   EMBO J. 4 (7), 1755-1759 (1985)
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ORIGIN

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Qy       1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
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Db        961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy       1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy       1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy       1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy       1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy       1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy       1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy       1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy       1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db       1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy       1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy       1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy       1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy       2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy       2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy       2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy       2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy       2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy       2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy       2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy       2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

Qy       2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

Qy       2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy       2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

Qy       2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy       2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy       2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

Qy       2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

Qy       2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

Qy       3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy       3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy       3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy       3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy       3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy       3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy       3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy       3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy       3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db       3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy       3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy       3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy       3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy       3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy       3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy       3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
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Db       3541 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600
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Qy   3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
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Db   3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy   4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
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Qy   4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
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Db   3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy   4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
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Db   3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy   4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
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Db   3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy   4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
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Qy   4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
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Db   4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy   4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
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Db   4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy   4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
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Db   4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy   4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
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Db   4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy   4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
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Qy   4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
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Db   4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy   4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
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Db   4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy   4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy   4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy   4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
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Qy   4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
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Qy   5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
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Db   4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy   5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
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Qy   5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
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Db   4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy   5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy   5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
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Db   4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

Qy   5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
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Db   4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy   5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
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Qy   5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy   5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
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Db   5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy   5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy   5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
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Db   5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy   5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
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Db   5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy   5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
          ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy   5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
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Qy   5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
          |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db   5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

Qy   5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

Qy   5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy   6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
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Db   5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy   6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
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Qy       6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
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Db       5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy       6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
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Db       5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy       6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
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Db       6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy       6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
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Qy       6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
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Qy       6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
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Db       6181 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

Qy       6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
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Qy       6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
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Qy       6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
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Db       6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

Qy       6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
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Db       6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

Qy       6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
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Db       6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

Qy       6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
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Db       6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

Qy       6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
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Qy       7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
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Qy       7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
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Qy       7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
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Qy       7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
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Qy       7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
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Qy       7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
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Qy       7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
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Qy       7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
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Qy       7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
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Qy       7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
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Qy       7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
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Db       7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

Qy       7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
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Db       7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy       7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
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Qy       7789 CAGTACT 7795
              |||||||
Db       7441 CAGTACT 7447


RESULT 13
A14133
LOCUS       A14133                  7705 bp    DNA     linear   PAT 30-NOV-1994
DEFINITION  Fibronectin gene.
ACCESSION   A14133
VERSION     A14133.1  GI:490127
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 7705)
  AUTHORS   Baralle,F.E.
  TITLE     Fibronectins
  JOURNAL   Patent: EP 0207751-A 2 07-JAN-1987;
            Delta Biotechnology Limited
FEATURES             Location/Qualifiers
     source          1. .7705
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     misc_feature    5. .6985
                     /note="CDS, fibronectin gene"
     misc_feature    647. .649
                     /note="the sequence given is TGA, but the codon is shown
                     in the specification as encoding Glycine for which the
                     correct codon is GGN"
ORIGIN

  Query Match             95.2%;  Score 7418.2;  DB 6;  Length 7705;
  Best Local Similarity   99.8%;  Pred. No. 0;
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Matches 7429;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy    349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy    409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy    469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
          |||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db    121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy    529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

Qy    589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

Qy    649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy    709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy    769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
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Db    421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480

Qy    829 TGATCATGCTGCTGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
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Qy    889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
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Db    541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy    949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
          |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db    601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTTGAGACACCTGGAG 660

Qy   1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy   1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
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Db    721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy   1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
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Db    781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy   1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG 1248
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Db    841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGTTGAAGACACAAGG 900

Qy   1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy   1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy   1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy   1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy   1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
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Db   1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy   1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
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Db   1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy   1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
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Db   1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy   1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy   1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
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Qy   1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy   1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
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Db   1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy   1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
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Db   1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy   1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
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Db   1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy   2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
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Db   1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy   2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
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Db   1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy   2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
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Db   1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy   2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
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Db   1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy   2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
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Db   1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy   2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
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Db   1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy   2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
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Db   2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy   2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
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y         2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
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b         2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

y         2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
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b         2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

y         2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
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y         2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
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y         2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
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b         2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

y         2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
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b         2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

y         2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
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b         2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

y         2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

y         3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

y         3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

y         3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

y         3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

y         3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

y         3349 CCGACTGACCGTGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
               ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
b         3001 CCGACTGACCGTGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

y         3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
               ||||| ||||||||| ||||||||||||||||||||||||||||||||||||||||||||
b         3061 TGTCTTCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

y         3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

y         3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
               |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
b         3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

y         3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy        3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy        3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy        3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy        3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy        4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy        4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy        4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy        4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy        4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy        4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy        4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy        4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4261 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4320

Qy        4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy       4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy       4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy       4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy       4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

Qy       4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

Qy       5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy       5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800

Qy       5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy       5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy       5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
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Db       4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

Qy       5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy       5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy       5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy       5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy       5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy       5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
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Qy       5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy       5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy       5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5461 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5520

Qy       5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
              |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db       5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

Qy       5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

Qy       5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy       6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy       6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

Qy       6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

Qy       6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy       6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy       6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy       6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy       6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

Qy       6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6181 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

Qy       6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360

Qy       6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

Qy       6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db       6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

Qy       6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540
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y         6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

y         6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

y         7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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y         7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

y         7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         6781 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840

y         7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         6841 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 6900

y         7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960

y         7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

y         7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080

y         7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

y         7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

y         7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260

y         7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
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b         7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

y         7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
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y         7789 CAGTACT 7795
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R034630
OCUS       AR034630                   7705 bp    DNA     linear   PAT 29-SEP-1999
EFINITION  Sequence 16 from patent US 5869616.
CCESSION   AR034630
ERSION     AR034630.1  GI:5950235
EYWORDS    .
OURCE      Unknown.
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  ORGANISM  Unknown.
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REFERENCE   1  (bases 1 to 7705)
  AUTHORS   Vogel,T., Levanon,A., Werber,M.M.; Guy,R., Panet,A., Hartman,J. and
            Shaked,H.
  TITLE     Fibrin binding domain polypeptides and uses and methods of
            producing same
  JOURNAL   Patent: US 5869616-A 16 09-FEB-1999;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             95.2%;  Score 7418.2;  DB 6;  Length 7705;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7429;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy        349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
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Qy        409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
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Qy        469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
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Db        241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

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Qy        709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
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Qy        829 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
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Qy       1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGATGCAGTGGCTGAAGACACAAGG 1248
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Qy       3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
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Qy       3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
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y         3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
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Db        4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy        4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
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Qy        4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
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Qy        4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
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Qy        4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
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Qy        5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
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Qy        5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
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Qy        5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
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Qy        5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
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Qy        5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
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Qy        5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
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Db        5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy        5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
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Qy       5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
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Qy       5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
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Qy       5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
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Qy       5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
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Qy       5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
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Db       6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy       6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
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y        7789 CAGTACT 7795
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CCESSION   E01162
ERSION     E01162.1  GI:2169421
EYWORDS    JP 1987089699-A/1.
OURCE      Homo sapiens (human)
 ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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EFERENCE   1  (bases 1 to 7705)
 AUTHORS   Furanshisuko,I.B.
 TITLE     FIBRONECTIN
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RIGIN

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y         349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
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b           1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

y         409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
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y         469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
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y         529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
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Qy        589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy       1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy       1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy       1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320
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Qy   1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGATAAGCA 1728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGATAAGCA 1380

Qy   1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy   1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy   1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy   1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy   1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy   2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy   2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy   2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy   2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy   2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy   2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy   2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy   2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

Qy   2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

Qy   2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy   2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

Qy   2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy   2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy   2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

Qy   2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

Qy   2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

Qy   2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

Qy   3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy   3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy   3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy   3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy   3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy   3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy   3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
          ||||| ||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   3061 TGTCTTCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy   3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy   3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy   3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy   3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy   3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy   3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy   3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy          3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3541 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600

Qy          3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy          4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy          4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy          4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy          4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy          4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy          4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy          4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy          4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy          4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy          4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy          4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4261 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4320

Qy          4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy          4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy          4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy          4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy          4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

Qy          4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

Qy          5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy          5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800

Qy          5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy          5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy          5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

Qy          5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy          5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy          5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy          5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
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Db          5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy          5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy          5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy          5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy          5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
                 ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db          5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy          5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5461 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5520

Qy          5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
                 |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db          5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

Qy          5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

Qy          5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700
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Qy   6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy   6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

Qy   6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
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Db   5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

Qy   6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
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Db   5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy   6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
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Db   5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy   6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
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Qy   6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
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Qy   6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
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Qy   6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
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Qy   6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
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Qy   6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
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Qy   6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
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Qy   6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
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Qy   6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
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Qy   7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
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Qy   7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
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          |||||||
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                Copyright (c) 1993 - 2004  Compugen Ltd.

M nucleic - nucleic search, using sw model

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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                   SUMMARIES
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Result           Query
  No.   Score   Match Length DB  ID                           Description
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    1   930.6    72.6   1059  14  CF455952                    CF455952 AGENCOURT
    2   926.4    72.3   1150  9  AL527917                    AL527917 AL527917
    3     900    70.3   1201  9  AL554310                    AL554310 AL554310
    4   884.4    69.0   1080  12  BM808695                    BM808695 AGENCOURT
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        5   858.2    67.0    885  13  BU167861                 BU167861 AGENCOURT
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        7   834.6    65.2    966  13  BQ057770                 BQ057770 AGENCOURT
        8   833.2    65.0    888  13  BU147264                 BU147264 AGENCOURT
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c      10   827.4    64.6   1109  9  AL527916                 AL527916 AL527916
c      11   826.2    64.5    941  13  BX402738                 BX402738 BX402738
       12   823.2    64.3    953  13  BQ675847                 BQ675847 AGENCOURT
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       14   816.8    63.8   1045  13  BQ061207                 BQ061207 AGENCOURT
       15   816.4    63.7   1031  9  AL526453                 AL526453 AL526453
       16     813    63.5    825  12  BG740928                 BG740928 602634533
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       18   805.2    62.9    982  12  BM808219                 BM808219 AGENCOURT
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       20   800.6    62.5    923  13  BQ881755                 BQ881755 AGENCOURT
       21   795.4    62.1    797  12  BG741754                 BG741754 602633144
       22   790.2    61.7   1019  13  BQ066611                 BQ066611 AGENCOURT
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       25   778.8    60.8    925  12  BG740709                 BG740709 602631562
       26   778.4    60.8    870  14  CD246096                 CD246096 AGENCOURT
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       29     770    60.1    821  14  CD519378                 CD519378 AGENCOURT
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       39   744.8    58.1   1105  12  BG701638                 BG701638 602682528
       40   743.6    58.0    864  12  BG675145                 BG675145 602621420
       41   732.4    57.2    746  12  BG740126                 BG740126 602630724
       42     731    57.1    823  12  BG476978                 BG476978 602522210
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                                  ALIGNMENTS

RESULT 1
CF455952
LOCUS       CF455952                1059 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  AGENCOURT_15364423 Human Anterior Horn Homo sapiens cDNA clone
            IMAGE:30515595 5', mRNA sequence.
ACCESSION   CF455952
VERSION     CF455952.1  GI:34455608
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1059)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
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            http://image.llnl.gov
            Plate: NDAM580  row: p  column: 04
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FEATURES             Location/Qualifiers
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                     Invitrogen."
ORIGIN

  Query Match             72.6%;  Score 930.6;  DB 14;  Length 1059;
  Best Local Similarity   98.2%;  Pred. No. 6.3e-211;
  Matches  972;  Conservative    0;  Mismatches   15;  Indels    3;  Gaps    3;

Qy        295 GCGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGA 354
              | |  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         28 GGGATCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGA 87

Qy        355 GGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCT 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        415 GTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGA 474
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Db        148 GTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGA 207

Qy        475 ACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCC 534
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Db        208 ACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCC 267

Qy        535 GCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGG 594
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Qy        595 GCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGT 654
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Qy        655 TTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCC 714
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Db        388 TTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCC 447

Qy        715 GACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCC 774
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Qy        775 TGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGG 834
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Qy        835 AGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTA 894
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Qy        895 GGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATGGGGGTGTCC 954
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Qy        955 CCCGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTG 1014
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Qy       1015 GATATTGGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTCTCCATGGGGAAGACAGCCA 1074
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Qy       1075 TGCTCTTCAGGAGGAGACTCCAAGGGCAAA-GGAGGGTGTCTTGGCTGTGCTTGAAGGCG 1133
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Qy       1194 GGATGTTCTCAGCCCC-TTGTTCTGGGCAAGAACCCAGAGCTCCCC-AGTGTGGATACTA 1251
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Db        928 GGATGTTCTCAGCCCCTTTGTTCTGGGCCAGAACCCAAAGCTCCCCAATTGTGGATACTA 987

Qy       1252 ATAAACCTCTTGGAGCACAAAAAAAAAAAA 1281
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RESULT 2
AL527917
LOCUS       AL527917                1150 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  AL527917 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC027YM23 5-PRIME, mRNA sequence.
ACCESSION   AL527917
VERSION     AL527917.2  GI:31065768
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1150)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12791410.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 530.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DC027AG12QP1&cluster=530.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DC027AG12QP1.
FEATURES             Location/Qualifiers
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                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             72.3%;  Score 926.4;  DB 9;  Length 1150;
  Best Local Similarity   95.7%;  Pred. No. 6.4e-210;
  Matches  999;  Conservative   15;  Mismatches   21;  Indels    9;  Gaps    6;

Qy        239 GGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGG 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 GGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGG 126

Qy        299 CCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAA 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         127 CCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAA 186

y         359 ATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGC 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         187 ATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGC 246

y         419 TGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTT 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         247 TGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTT 306

y         479 CCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTG 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         307 CCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTG 366

y         539 GGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCAT 598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         367 GGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCAT 426

y         599 CTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCG 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         427 CTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCG 486

y         659 GGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACA 718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         487 GGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACA 546

y         719 GCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGA 778
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
b         547 GCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAACGTGGCCTGGA 606

y         779 CAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGA 838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         607 CAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGA 666

y         839 GCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAG 898
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         667 GCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAG 726

y         899 TGAGCTGGGGCCTGCTGAGGTGGGGGTGGGCTGACTCTGCAAAATGGGGGTGTCCCCCG 958
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
b         727 TGAGCTGGGGCCTGCTGAGGTGGGGGTGGGCTGACTCTGCAAAATGGGGGTGT-CCCCG 785

y         959 ATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATA 1018
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         786 ATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATA 845

y        1019 TTGGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTCTCCATGG-GGAAGACAGCCATGC 1077
              ||||||||||||||||||||||||||||||||||||||||||:| |||||||||||||||
b         846 TTGGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTCTCCATKGTGGAAGACAGCCATGC 905

y        1078 TCTTCAGGAGGAGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAAC 1137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         906 TCTTCAGGAGGAGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAAC 965

y        1138 CCTGCCATATCCCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGAT 1197
              |||||||||||||||:|:||||| |||:|: |||||||||||| |:||||||||||||:|
b         966 CCTGCCATATCCCCASTKCCAGT-CCCYCMACCTGTGGTGGCC-TKCATCCTGACTGGRT 1023

y        1198 GTTCTCAGCCCCTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGTGGATACTAATAAAC 1257
              |||||:| :|||||||||||||||| | |    |    |||: | ||||||:|||:||
b        1024 GTTCTMA-SCCCTTGTTCTGGGCAAAACC----AAACTCCCMATTTGGATAMTAAWAACT 1078

y        1258 CTCTTGGAGCACAAAAAAAAAAAA 1281
              ||    |:    :   |:||||||||
b        1079 CTTGGAGMAAYYTYARAAAAAAAA 1102


RESULT 3
AL554310
LOCUS       AL554310                1201 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL554310 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI082YA10 5-PRIME, mRNA sequence.
ACCESSION   AL554310
VERSION     AL554310.2  GI:31276123
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12894967.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 530.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI082BA05QP1&cluster=530.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI082BA05QP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             70.3%;  Score 900;  DB 9;  Length 1201;
  Best Local Similarity   97.2%;  Pred. No. 1.3e-203;
  Matches  931;  Conservative    5;  Mismatches   20;  Indels    2;  Gaps    2;

Qy         56 GGGAGGCTGCTCTGTGAAGGAACCGCCTTTCTCTCCGCGTGTCTCACCCTTTTCTCCCCA 115
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GGGATGCTGCTCTGTGAAGGAACCGCCTTTCTCTCCGCGTGTCTCACCCTTTTCTCCCCA 122

Qy        116 TATCTGTTTGGACATGAGCTGAGGGCACGGTCGCGGGCGGTCAGCCCTGTTCGCAGCTAC 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TATCTGTTTGGACATGAGCTGAGGGCACGGTCGCGGGCGGTCAGCCCTGTTCGCAGCTAC 182

Qy        176 GGCGAGGAGGGGCGCGATTGTTCCTTGTTGCCGCTCCGCTTAGTGGCCGCGTCCATTCCG 235
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        183 GGCGAGGAGGGGCGCGATTGCTCCTTGTTGCCGCTCCGCTTAGTGGCCGCGTCCATTCCG 242

Qy        236 CGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGG 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 CGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGG 302

Qy        296 CGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAG 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAG 362

Qy        356 GAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTG 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTG 422

Qy        416 TGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAA 475
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 TKCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAA 482

Qy        476 CTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCG 535
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 CTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCG 542
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Qy        536 CTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGG 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGG 602

Qy        596 CATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTT 655
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 CATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTT 662

Qy        656 TCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCG 715
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        663 TCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCG 722

Qy        716 ACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCT 775
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 ACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCT 782

Qy        776 GGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGA 835
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGA 842

Qy        836 GGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAG 895
              ||||||||||||| |:||||||||||||||||||||||||||||||||||||||||||||
Db        843 GGAGCAGTTGGAG-AMCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAG 901

Qy        896 GAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGCTGACTCTGCAAAATGGGGGTGTCCC 955
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        902 GAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGCTGACTCTGCAAAATGGGGGTGT-CC 960

Qy        956 CCGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGT 1013
              ||||||||||||||||||||||:   :  |||||  |  |  |   | || :|| | |
Db        961 CCGATCCTGGCCGAGGTGAGGAMAGAMAGGGGGGTCTARATYTGARGGGGTKGTGGAT 1018

RESULT 4
BM808695
LOCUS       BM808695                1080 bp    mRNA    linear   EST 05-MAR-2002
DEFINITION  AGENCOURT_6582590 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5471256
            5', mRNA sequence.
ACCESSION   BM808695
VERSION     BM808695.1  GI:19125506
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1080)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1979  row: g  column: 01
            High quality sequence start: 15
            High quality sequence stop: 695.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:5471256"
                     /tissue_type="amelanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
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                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             69.0%;  Score 884.4;  DB 12;  Length 1080;
  Best Local Similarity   97.4%;  Pred. No. 6.5e-200;
  Matches  962;  Conservative    0;  Mismatches   18;  Indels    8;  Gaps    6;

Qy        302 CATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATC 361
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db         27 CATGGCCCCGCTGGGATGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATC 86

Qy        362 CGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGT 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 CGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGT 146

Qy        422 CCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 CCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCA 206

Qy        482 GAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGG 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGG 266

Qy        542 AGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTC 601
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Db        267 AGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTC 326

Qy        602 CCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGA 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 CCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGA 386

Qy        662 GGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCA 721
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Db        387 GGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCA 446

Qy        722 GCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAA 781
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Qy        782 CTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCA 841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 CTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCA 566

Qy        842 GTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGA 901
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Db        567 GTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGA 626

Qy        902 GCTGGGGCCTGCTGAGGTGGGGGTGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATC 961
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Db        627 GCTGGGGCCTGCTGAGGTGGGGGTGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATC 686

Qy        962 CTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTG 1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 CTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTG 746

Qy       1022 GGCAAGGCA-GGAAACCTCTGGAGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCT 1080
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Db        747 GGCAAGGCAGGGAAACCTCTGGAGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCT 806

Qy       1081 TCAGGAGGAGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCT 1140
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Db        807 TCAGGAGGAGACTNCANGGGCAAAGGAGGGTGTCTTGGCTGTGCTTTGAAGCGAAACCCT 866

Qy       1141 GCCATATCCCCAGTGCCAGTCCCCTCAGCCT-GTGGTGGCCTTGCA-TCCTGACTGGATG 1198
              ||||||||||||||||||||||||||||||| ||||||||||||| ||||||||||||||
Db        867 GCCATATCCCCAGTGCCAGTCCCCTCAGCCTGGTGGTGGCCTTGCATTCCTGACTGGATG 926

Qy       1199 TTCTCAGCCCC--TTGTTCTGGGCAAGAACCCAGAGCTCCCCAGT-GTGGATACTAATAA 1255
              ||||  |||||  |  |   |||||||| |||||| ||||||||| ||||||||||||||
b         927 TTCTTCGCCCCCTTGTTCTGGGGCAAGACCCCAGAACTCCCCAGTGGTGGATACTAATAA 986

y        1256 A--CCTCTTGGAGCACAAAAAAAAAAAA 1281
              |  |||||||||||   |||||||||||
b         987 AACCCTCTTGGAGCCTCAAAAAAAAAAA 1014


ESULT 5
U167861
OCUS       BU167861                  885 bp    mRNA    linear   EST 04-SEP-2002
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CCESSION   BU167861
ERSION     BU167861.1  GI:22681845
EYWORDS    EST.
OURCE      Homo sapiens (human)
 ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
EFERENCE   1  (bases 1 to 885)
 AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
 TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL   Unpublished (1999)
OMMENT     Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM2328  row: f  column: 04
           High quality sequence stop: 667.
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                    /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                    EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                    into EcoRI/XhoI sites using the following 5' adaptor:
                    GGCACGAG(G). Library constructed by Ling Hong in the
                    laboratory of Gerald M. Rubin (University of California,
                    Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                    Superscript II RT (Life Technologies). Note: this is a
                    NIH_MGC Library."
RIGIN

  Query Match             67.0%;  Score 858.2;  DB 13;  Length 885;
  Best Local Similarity   98.5%;  Pred. No. 1.1e-193;
  Matches  866;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

y          51 ACGAGGGGAGGCTGCTCTGTGAAGGAACCGCCTTTCTCTCCGCGTGTCTCACCCTTTTCT 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           1 ACGAGGGGAGGCTGCTCTGTGAAGGAACCGCCTTTCTCTCCGCGTGTCTCACCCTTTTCT 60

y         111 CCCCATATCTGTTTGGACATGAGCTGAGGGCACGGTCGCGGGCGGTCAGCCCTGTTCGCA 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCCATATCTGTTTGGACATGAGCTGAGGGCACGGTCGCGGGCGGTCAGCCCTGTTCGCA 120

y         171 GCTACGGCGAGGAGGGGCGCGATTGTTCCTTGTTGCCGCTCCGCTTAGTGGCCGCGTCCA 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTACGGCGAGGAGGGGCGCGATTGTTCCTTGTTGCCGCTCCGCTTAGTGGCCGCGTCCA 180

Qy        231 TTCCGCGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGG 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCCGCGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGG 240
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Qy        291 CGTGGCGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGC 350
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Db        241 CGTGGCGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGC 300

Qy        351 AAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGAT 410
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Db        301 AAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGAT 360

Qy        411 GTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGC 470
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Qy        471 TTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATG 530
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Db        421 TTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATG 480

Qy        531 ATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTG 590
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Db        481 ATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTG 540

Qy        591 GAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAG 600

Qy        651 TGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAG 710
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Db        601 TGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAG 660

Qy        711 AGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGT 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        771 GGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGC 830
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Db        721 GGCCTGGACCACTTCGGGGACTTTGACTGGGTCATCGAGAACCCTGGAGTTGAACACCGC 780

Qy        831 CTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGT 890
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Db        781 CTGGAGGAGCAGTTGGAGAACCTGATAAAATTTATCCGCTCCAGACTTTAGTCACTAGGT 840

Qy        891 TCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGG 929
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Db        841 TCTAGGAGTGAGCTGGGGCCCTGCTAAGGGGGGGGGTGG 879


RESULT 6
BQ888524
LOCUS       BQ888524                  909 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8071320 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6090682
            5', mRNA sequence.
ACCESSION   BQ888524
VERSION     BQ888524.1  GI:22280538
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 909)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2332  row: h  column: 11
            High quality sequence stop: 641.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:6090682"
                     /tissue_type="melanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_112"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             65.2%;  Score 834.8;  DB 13;  Length 909;
  Best Local Similarity   97.7%;  Pred. No. 4.2e-188;
  Matches  868;  Conservative    0;  Mismatches   17;  Indels    3;  Gaps    2;

Qy         51 ACGAGGGGAGGCTGCTCTGTGAAGGAACCGCCTTTCTCTCCGCGTGTCTCACCCTTTTCT 110
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Qy        111 CCCCATATCTGTTTGGACATGAGCTGAGGGCACGGTCGCGGGCGGTCAGCCCTGTTCGCA 170
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Qy        171 GCTACGGCGAGGAGGGGCGCGATTGTTCCTTGTTGCCGCTCCGCTTAGTGGCCGCGTCCA 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        231 TTCCGCGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGG 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCCGCGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGG 240

Qy        291 CGTGGCGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGC 350
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Qy        351 AAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGAT 410
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Qy        411 GTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGC 470
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Qy        531 ATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTG 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTG 540

Qy        591 GAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAG 650
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Db        541 GAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAG 600

Qy        651 TGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAG 710
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Qy        711 AGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGT 770
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Qy        771 GGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGC 830
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Db        781 CTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCCTCCAGACTTTAGTCACTAGG 840

Qy        888 GGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACT 935
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Db        841 GGTCTAGGAAGTGAGCTGGGGCCTGCCTTAAAGGGGGGGTGGGGCCT 888


RESULT 7
BQ057770
LOCUS       BQ057770                 966 bp    mRNA    linear   EST 29-MAR-2002
DEFINITION  AGENCOURT_7047170 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5813479
            5', mRNA sequence.
ACCESSION   BQ057770
VERSION     BQ057770.1  GI:19817110
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 966)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2065  row: j  column: 08
            High quality sequence stop: 705.
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_99"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
ORIGIN

  Query Match             65.2%;  Score 834.6;  DB 13;  Length 966;
  Best Local Similarity   98.2%;  Pred. No. 4.8e-188;
  Matches  865;  Conservative    0;  Mismatches   14;  Indels    2;  Gaps    2;

Qy        403 GAGCTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGG 462
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Db          1 GAGCTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGG 60

Qy        463 AGCATGGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGA 522
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Qy        523 AGGACATGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGA 582
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Qy        583 AGATTGTGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTG 642
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Qy        823 AACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGT 882
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Db        421 AACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGT 480

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Db        601 AGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTCTCCATGG 660

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Db        781 GCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCCAGAGCCTCCCCAGT 840

Qy       1242 GT-GGATACTAATAAACCTCTTGGAGCACAAAAAAAAAAAA 1281
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Db        841 GTGGGATACTAAATAAACCCTCTTGGAGCCCCAAAAAAAA 881
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RESULT 8
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LOCUS       BU147264               888 bp    mRNA    linear   EST 03-SEP-2002
DEFINITION  AGENCOURT_8070801 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6089738
            5', mRNA sequence.
ACCESSION   BU147264
VERSION     BU147264.1  GI:22660796
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 888)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2330  row: a  column: 03
            High quality sequence stop: 698.
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_112"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             65.0%;  Score 833.2;  DB 13;  Length 888;
  Best Local Similarity   98.2%;  Pred. No. 1e-187;
  Matches  864;  Conservative    0;  Mismatches   13;  Indels    3;  Gaps    2;

Qy         51 ACGAGGGGAGGCTGCTCTGTGAAGGAACCGCCTTTCTCTCCGCGTGTCTCACCCTTTTCT 110
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Db          1 ACGAGGGGAGGCTGCTCTGTGAAGGAACCGCCTTTCTCTCCGCGTGTCTCACCCTTTTCT 60

Qy        111 CCCCATATCTGTTTGGACATGAGCTGAGGGCACGGTCGCGGGCGGTCAGCCCTGTTCGCA 170
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Db         61 CCCCATATCTGTTTGGACATGAGCTGAGGGCACGGTCGCGGGCGGTCAGCCCTGTTCGCA 120

Qy        171 GCTACGGCGAGGAGGGGCGCGATTGTTCCTTGTTGCCGCTCCGCTTAGTGGCCGCGTCCA 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTACGGCGAGGAGGGGCGCGATTGTTCCTTGTTGCCGCTCCGCTTAGTGGCCGCGTCCA 180

Qy        231 TTCCGCGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGG 290
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Db        181 TTCCGCGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGG 240

Qy        291 CGTGGCGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGC 350
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Qy        351 AAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGAT 410
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Db        301 AAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGAT 360

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Db        421 TTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATG 480

Qy        531 ATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTG 590
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Db        481 ATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTG 540

Qy        591 GAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAG 650
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Db        541 GAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAG 600

Qy        651 TGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAG 710
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Db        601 TGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAG 660

Qy        711 AGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGT 770
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Qy         771 GGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGC 830
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Qy         831 CTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCT-CCAGACTTTAGTCACTAGG 889
               |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||| |
Db         781 CTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCCAGACTTTAGTCACTAAG 840

Qy         890 TT--CTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGG 927
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Db         841 TTTCTAGGAACTGAGCTGGGGCCTGCTTTAAGGTGGGGGG 880


RESULT 9
BM423359
LOCUS       BM423359                1059 bp    mRNA    linear   EST 29-JAN-2002
DEFINITION  AGENCOURT_6402244 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5516495
            5', mRNA sequence.
ACCESSION   BM423359
VERSION     BM423359.1  GI:18391584
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1059)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2017  row: c  column: 24
            High quality sequence stop: 681.
FEATURES             Location/Qualifiers
     source          1..1059
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5516495"
                     /tissue_type="amelanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_41"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             65.0%;  Score 833;  DB 12;  Length 1059;
  Best Local Similarity   98.1%;  Pred. No. 1.2e-187;
  Matches  874;  Conservative    0;  Mismatches   12;  Indels    5;  Gaps    3;

Qy         303 ATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCC 362
               ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGGCCCCGCTGGGATGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCC 60

Qy         363 GGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTC 422
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTC 120

Qy         423 CTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAG 482
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAG 180

Qy         483 AGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGA 542
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 AGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGA 240

Qy         543 GAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCC 602
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCC 300

Qy         603 CAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAG 662
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 CAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAG 360

Qy         663 GCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCAG 722
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCAG 420

Qy         723 CGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAAC 782
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 CGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAAC 480

Qy         783 TTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAG 842
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 TTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAG 540

Qy         843 TTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAG 902
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAG 600

Qy         903 CTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATCC 962
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 CTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATCC 660

Qy         963 TGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGG--GGTTGGTGGATATT 1020
               ||||||||||||||||||||||||||||||||||||||||| ||  ||||||||||||||
Db         661 TGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGANGGNNGGTTGGTGGATATT 720

Qy        1021 GGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCT 1080
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Db         721 GGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCT 780

Qy        1081 TCAGGAGGAGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTGT--GCTTGAAGGCGAAACC 1138
               |||||||||||||||| ||  || ||||||||||||||||||    |  | | |||||||
Db         781 TCAGGAGGAGACTCCAGGGCAAAGGGAGGGTGTCTTGGCTGTTGCTTGAANGCCGAAACC 840

Qy        1139 CTGCCATATCCCCAGTGCCAGTCCCCT-CAGCCTGTGGTGGCCTTGCATCC 1188
               ||||||||||||||||||||||||||| |||||||||||||||||||||||
Db         841 CTGCCATATCCCCAGTGCCAGTCCCCTCCAGCCTGTGGTGGCCTTGCATCC 891


RESULT 10
AL527916/c
LOCUS       AL527916                1109 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  AL527916 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC027YM23 3-PRIME, mRNA sequence.
ACCESSION   AL527916
VERSION     AL527916.2  GI:31065767
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1109)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12791409.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
```

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               Library was constructed by Life Technologies, a division of
               Invitrogen. This sequence belongs to sequence cluster 530.f For
               more information about this cluster, see
               http://www.genoscope.cns.fr/
               cgi-bin/cluster.cgi?seq=CS0DC027AG12NP1&cluster=530.f. Contact :
               Feng Liang Email : fliang@lifetech.com URL :
               http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
               Faraday Avenue Genoscope sequence ID : CS0DC027AG12NP1.
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    source               1. .1109
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                         /db_xref="taxon:9606"
                         /clone="CS0DC027YM23"
                         /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
                         /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
                         /note="1st strand cDNA was primed with a NotI-oligo(dT)
                         primer. Five prime end enriched, double-strand cDNA was
                         digested with Not I and cloned into the Not I and EcoR V
                         sites of the pCMVSPORT 6 vector. Library was normalized."
RIGIN

  Query Match             64.6%;  Score 827.4;  DB 9;  Length 1109;
  Best Local Similarity   94.2%;  Pred. No. 2.6e-186;
  Matches  844;  Conservative    8;  Mismatches   44;  Indels    0;  Gaps    0;

y          347 CGGCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGC 406
               | :| . ||  ||  | |||| || :||||:|||:||| ||||:|||||| |||||| ||
b          908 CASCGCAAGAGAAATCCGGAAAGAAYTCGTVACCSAGGGGCTGMAGAGCAAACTTGGGGC 849

y          407 TGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCA 466
               ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
b          848 TGATGTCTGGGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCA 789

y          467 TGGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGA 526
               ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||| |
b          788 TGGCTTGAACTTCCAGAGACTCCTGAACACCAGCACCTACAAGGAGGCCTTTCGGAAGAA 729

y          527 CATGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGAT 586
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          728 CATGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGAT 669

y          587 TGTGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACAT 646
               |||||||||||||||||||||||||||||||||:||| |||||||||||||||||:||||
b          668 TGTGGAGGGCATCTCCCAGCCCATCTGGCTGGTRAGTAACACACGGAGAGTGTCTRACAT 609

y          647 CCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGA 706
               |||||||||||||:|||||||||||||| | |||||||||||||||||||||||||||||
b          608 CCAGTGGTTTCGGRAGGCCTATGGGGCCATAACGCAGACGGTCCGCGTTGTAGCGTTGGA 549

y          707 GCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGA 766
               ||||||||||||||||||||||||||||||||| |||||||||||||||||| |||||||
b          548 GCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACCCCAGGGGTGGACGATGCTNAGTCAGA 489

y          767 ATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACA 826
               | |||||||| ||||||||||||||||| |||||||||||||||||||||||||||||||
b          488 ACGTGGCCTGNACAACTTCGGGGACTTTNACTGGGTCATCGAGAACCATGGAGTTGAACA 429

y          827 GCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACT 886
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Db         428 GCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAAACTTTAGTCACT 369

Qy         887 AGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATGG 946
               ||||||||||||||||||||| |||||| |||||||||||||||| ||||||||||||||
Db         368 AGGTTCTAGGAGTGAGCTGGGNCCTGCTAAGGTGGGGGTGGGGCTAACTCTGCAAAATGG 309

Qy         947 GGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGG 1006
               |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db         308 GGGTGTCCCCCGATCCTGGCCGAGGTGAGGNACAGACAGGGGGGGTCTAGATTCTGAGGG 249

Qy        1007 GGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTCTCCATGGGGAA 1066
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        1067 GACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTGCTT 1126
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Db         188 NACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTGCTT 129

Qy        1127 GAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCAT 1186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         128 GAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCAT 69

Qy        1187 CCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTG 1242
               ||| ||||||||||||||||||||||||||| |||| | ||     | ||   |||
Db          68 CCTNACTGGATGTTCTCAGCCCCTTGTTCTGNGCAAAACCCAGNGTCCCCAGTGTG 13


RESULT 11
BX402738/c
LOCUS       BX402738                 941 bp    mRNA    linear   EST 13-MAY-2003
DEFINITION  BX402738 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI082YA10 3-PRIME, mRNA sequence.
ACCESSION   BX402738
VERSION     BX402738.1  GI:30630798
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 941)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 530.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS1AI021ZC06NP1&cluster=530.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS1AI021ZC06NP1.
FEATURES             Location/Qualifiers
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                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             64.5%;  Score 826.2;  DB 13;  Length 941;
  Best Local Similarity   93.3%;  Pred. No. 4.8e-186;
  Matches  878;  Conservative    7;  Mismatches   52;  Indels    4;  Gaps    4;

Qy         297 GGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGG 356
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Db         941 GGCCCWATGKCYCCGYTGGGAGTCTCCCCGCGTCTKGSACTTCTTTTCWGCGGCAAGAGG 882

Qy         357 AAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGT 416
               |||||||||||||||||||||||||||||| :|||||||||||||||||||||||||||:
Db         881 AAATCCGGGAAGGACTTCGTGACCGAGGCG-YGCAGAGCAGACTTGGAGCTGATGTCTGK 823

Qy         417 GCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAAC 476
               ||||||  | |       |  |||| |||||||||| |||| |||||||||||| |||||
Db         822 GCTGTCNCCGGNNCTCTNGNNCCACNCAAGGAACAGNATGCNCAGGAGCATGGC-TGAAC 764

Qy         477 TTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGC 536
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              |||||||||||| |||||||||||||| ||||||||||||||||||||||||||| ||||
Db       763 TTCCAGAGACTCNTGGACACCAGCACCNACAAGGAGGCCTTTCGGAAGGACATGANCCGC 704

Qy       537 TGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGC 596
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Db       703 TGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTC-TTTGCAGGAAGATAGTGGAGGGC 645

Qy       597 ATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTT 656
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Db       644 ATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACANCCAGTGGTTN 585

Qy       657 CGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCG-TTGTAGCGTTGGAGCAGAGCCG 715
             ||||||||||| ||||||| ||||||||||||||||| ||||||||||||||||||||||
Db       584 CGGGAGGCCTANGGGGCCGNGACGCAGACGGTCCGCGTTTGTAGCGTTGGAGCAGAGCCG 525

Qy       716 ACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCT 775
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Db       524 ACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCT 465

Qy       776 GGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGA 835
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Db       464 GGACAACTTCGGGGACTTTGACTGGGNCANCGAGAACCANGGAGTNGAACAGCGCCTGGA 405

Qy       836 GGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAG 895
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Db       404 GGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAG 345

Qy       896 GAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATGGGGGTGTCCC 955
             ||||||||||||||||||||||| ||||| ||||||||| | ||||||||||||||||||
Db       344 GAGTGAGCTGGGGCCTGCTGAGGNGGGGGNGGGGCTGACNCNGCAAAATGGGGGTGTCCC 285

Qy       956 CCGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGG 1015
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Db       284 CCGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGG 225

Qy      1016 ATATTGGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTCTCCATGGGGAAGACAGCCAT 1075
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Db       224 ATATTGGGCAAGGCAGGAAACNTCTGGAGACNTCATTTTCTCCATGGGGAAGACAGCCAT 165

Qy      1076 GCTCTTCAGGAGGAGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAA 1135
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       164 GCTCTTCAGGAGGAGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAA 105

Qy      1136 ACCCTGCCATATCCCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCATCCTGACTGG 1195
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Db       104 ACCCTGCCATATCCCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCATCCTGACTGG 45

Qy      1196 ATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCCAGAGCTCC 1236
             ||||||||||||| ||||| |||  |  |    |||| | |
Db        44 ATGTTCTCAGCCCNTTGTTNTGGNAAGAACGNNAGAGNTAC 4


RESULT 12
BQ675847
LOCUS       BQ675847                 953 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8062687 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6211288
            5', mRNA sequence.
ACCESSION   BQ675847
VERSION     BQ675847.1  GI:21786681
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 953)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2373  row: i  column: 17
            High quality sequence stop: 651.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_102"
                     /note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Library constructed
                     by Ling Hong in the laboratory of Gerald M. Rubin
                     (University of  California, Berkeley) using ZAP-cDNA
                     synthesis kit (Stratagene) and Superscript II RT (Life
                     Technologies). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             64.3%;  Score 823.2;  DB 13;  Length 953;
  Best Local Similarity   96.4%;  Pred. No. 2.5e-185;
  Matches  863;  Conservative    0;  Mismatches   29;  Indels    3;  Gaps    2;

Qy       100 CACCCTTTTCTCCCCATATCTGTTTGGACATGAGCTGAGGGCACGGTCGCGGGCGGTCAG 159
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Db         1 CACCCTTTTCTCCCCATATCTGTTTGGACATGAGCTGAGGGCACGGTCGCGGGCGGTCAG 60

Qy       160 CCCTGTTCGCAGCTACGGCGAGGAGGGGCGCGATTGTTCCTTGTTGCCGCTCCGCTTAGT 219
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Db        61 CCCTGTTCGCAGCTACGGCGAGGAGGGGCGCGATTGCTCCTTGTTGCCGCTCCGCTTAGT 120

Qy       220 GGCCGCGTCCATTCCGCGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAG 279
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Db       121 GGCCGCGTCCATTCCGCGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAG 180

Qy       280 GCATCGCGAGGCGTGGCGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGC 339
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Db       181 GCATCGCGAGGCGTGGCGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGC 240

Qy       340 TGTTCAGCGGCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGAC 399
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Db       241 TGTTCAGCGGCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGAC 300

Qy       400 TTGGAGCTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTC 459
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Db       301 TTGGAGCTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTC 360

Qy       460 AGGAGCATGGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTC 519
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Db       361 AGGAGCATGGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTC 420

Qy       520 GGAAGGACATGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCA 579
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Qy       640 CTGACATCCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAG 699
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Qy       700 CGTTGGAGCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTG 759
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Qy         760 AGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAG 819
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Qy         820 TTGAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTT 879
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         880 AGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGA--GGTGGGGGTGGGGCTGACTCT 937
               |||||||| ||||||| | ||||||||||||| ||||  |  ||||  |||| |||||||
Db         781 AGTCACTAAGTTCTAGTAATGAGCTGGGGCCTCCTGAAGGTGGGGGTGGGGGTTGACTCT 840

Qy         938 G-CAAAATGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGG 991
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Db         841 GCCAAAAGGGGGGGGCCCCCCCATCCTGGCCCCGGTGGACGAACAAAACCGGGCG 895


RESULT 13
BQ683855
LOCUS       BQ683855                 930 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8494813 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6294897
            5', mRNA sequence.
ACCESSION   BQ683855
VERSION     BQ683855.1  GI:21796534
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 930)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2500  row: e  column: 10
            High quality sequence start: 6
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FEATURES             Location/Qualifiers
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                     /clone="IMAGE:6294897"
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_112"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             63.8%;  Score 817.2;  DB 13;  Length 930;
  Best Local Similarity   97.3%;  Pred. No. 6.6e-184;
  Matches  895;  Conservative    0;  Mismatches   18;  Indels    7;  Gaps    6;

Qy          37 GGTGGGGGAGCTTCACGAGGGGAGGCTGCTCTGTGAAGGAACCGCCTTTCTCTCCGCGTG 96
               ||   | | |||||||||||||||||||||||||||||||||||||||||||||||||||
Db           9 GGCACGAGGGCTTCACGAGGGGAGGCTGCTCTGTGAAGGAACCGCCTTTCTCTCCGCGTG 68

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Qy         157 CAGCCCTGTTCGCAGCTACGGCGAGGAGGGGCGCGATTGTTCCTTGTTGCCGCTCCGCTT 216
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Qy         217 AGTGGCCGCGTCCATTCCGCGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTT 276
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Qy         277 CAGGCATCGCGAGGCGTGGCGGCCCCATGGCCCCGCTGGGAGGCGCCCCGCGGCTGGTAC 336
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Qy         337 TGCTGTTCAGCGGCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCA 396
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Db         309 TGCTGTTCAGCGGCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCA 368

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Db         369 GACTTGGAGCTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATG 428

Qy         457 CTCAGGAGCATGGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCT 516
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Db         429 CTCAGGAGCATGGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCT 488

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Db         549 GCAGGAAGATTGTGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAG 608

Qy         637 TGTCTGACATCCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTG 696
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Db         609 TGTCTGACATCCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTG 668

Qy         697 TAGCGTTGGAGCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCA-GGGGTGGACGAT 755
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Db         669 TAGCGTTGGAGCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGGGGGACGAT 728

Qy         756 GCTGAGTCAGAATGTGGCCTGGACAAC-TTCGGGGACTTTGACTGGGTCATCGAGAACCA 814
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Db         789 TGGAGTTGAACAGCGCCTGGAAGGAGCAGTTGGAGAACCTGAATAGAATTTATCCGCTCC 848

Qy         873 AGAC-TTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGA--GGTGGGGGTGGGG 929
               |||| ||||| |  ||||||||| |||||| |||||||||||| |  |  ||||  ||||
Db         849 AGACTTTTAGCCCTTAGGTTCTAAGAGTGACCTGGGGCCTGCTTAAGGTGGGGGTGGGGG 908

Qy         930 CTGACTCTGCAAAATGGGGG 949
               ||||||| || |||||||||
Db         909 CTGACTCGGCCAAATGGGGG 928


RESULT 14
BQ061207
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DEFINITION  AGENCOURT_6863200 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920244
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ACCESSION   BQ061207
VERSION     BQ061207.1  GI:19885042
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1045)
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  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2083  row: j  column: 21
            High quality sequence stop: 623.
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                     /lab_host="DH10B (phage-resistant)"
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                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
ORIGIN

  Query Match            63.8%;  Score 816.8;  DB 13;  Length 1045;
  Best Local Similarity   95.5%;  Pred. No. 8.5e-184;
  Matches  882;  Conservative    0;  Mismatches   36;  Indels    6;  Gaps    4;

Qy        364 GGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCC 423
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Qy        424 TCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGA 483
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Qy        484 GACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGAG 543
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Qy        724 GGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACT 783
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Qy        784 TCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGT 843
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Qy        844 TGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGC 903
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Db        481 TGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGC 540

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Db        721 GGAGGAGACTCCAGGGCAAAAGGAGGNTGTCNTGGCTGTGCTTTGAGGCGAAACCCTGCC 780

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Db        781 ATATCCCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCATTCCTGACTGGAGGGGTC 840

Qy       1202 TCAGCCCCTT-GTTCTGGGCAAGAACCCAGAGCTCCCC---AGTGTGGATACTAATAAAC 1257
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RESULT 15
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ACCESSION   AL526453
VERSION     AL526453.2  GI:31064311
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1031)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12789946.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 530.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DC014DF12QP1&cluster=530.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DC014DF12QP1.
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                     /clone="CS0DC014YL24"
                     /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
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ORIGIN
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  Query Match             63.7%;  Score 816.4;  DB 9;  Length 1031;
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Qy        524 GGACATGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAA 583
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Db        128 GGACATGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAA 187

Qy        584 GATTGTGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGA 643
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Qy        944 TGGGGGTGTCCCCCGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGA 1003
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Qy       1004 GGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTCTCCATGGG 1063
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Qy       1184 CATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGT 1243
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                        GenCore version 5.1.6
               Copyright (c) 1993 - 2004  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          March  7, 2004, 08:00:48 ; Search time 546 Seconds
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                                            7922.788 Million cell updates/sec

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Perfect score:   7795
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Scoring table:   IDENTITY_NUC
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Searched:        682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters:      1365418

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      Pred. No. is the number of results predicted by chance to have a
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    1    7780.6      99.8    8044  4  US-09-566-921-135             Sequence 135, App
    2      7423      95.2    7679  4  US-09-220-132-38              Sequence 38, Appl
    3      7423      95.2    7680  4  US-09-023-655-1289            Sequence 1289, Ap
    4      7423      95.2    7680  5  PCT-US95-09819-6              Sequence 6, Appli
    5    7418.2      95.2    7705  1  US-08-259-569-16              Sequence 16, Appl
    6    7418.2      95.2    7705  2  US-08-826-885-16              Sequence 16, Appl
    7    7413.4      95.1    7705  6  5455158-2                    Patent No. 5455158
    8      7223      92.7    7803  2  US-08-551-356-1               Sequence 1, Appli
    9      7223      92.7    7803  5  PCT-US93-12687-1              Sequence 1, Appli
   10    2211.8      28.4    4027  2  US-08-551-356-5               Sequence 5, Appli
   11    2211.8      28.4    4027  5  PCT-US93-12687-5              Sequence 5, Appli
   12      1400      18.0    2481  4  US-09-366-009-20              Sequence 20, Appl
   13      1400      18.0    2481  4  US-08-809-156B-20             Sequence 20, Appl
   14     921.2      11.8    1722  4  US-09-366-009-33              Sequence 33, Appl
   15     921.2      11.8    1722  4  US-08-809-156B-33             Sequence 33, Appl
   16     877.4      11.3    1416  4  US-09-366-009-27              Sequence 27, Appl
   17     877.4      11.3    1416  4  US-08-809-156B-27             Sequence 27, Appl
   18     860.8      11.0    1644  4  US-09-366-009-17              Sequence 17, Appl
   19     860.8      11.0    1644  4  US-08-809-156B-17             Sequence 17, Appl
   20       831      10.7    1374  4  US-09-366-009-26              Sequence 26, Appl
   21       831      10.7    1374  4  US-08-809-156B-26             Sequence 26, Appl
   22     766.4       9.8     986  1  US-07-637-250A-8              Sequence 8, Appli
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   24       652       8.4     653  4  US-09-404-879A-370            Sequence 370, App
   25       610       7.8     610  2  US-08-692-787-7               Sequence 7, Appli
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c  27       606       7.8     606  1  US-07-803-623B-10             Sequence 10, Appl
c  28       606       7.8     606  2  US-08-806-084-10              Sequence 10, Appl
c  29       606       7.8     606  4  US-09-201-970A-10             Sequence 10, Appl
c  30       606       7.8     691  4  US-09-404-879A-240            Sequence 240, App
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   38     604.4       7.8     606  5  PCT-US92-10511-1              Sequence 1, Appli
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                                   ALIGNMENTS


RESULT 1
US-09-566-921-135
; Sequence 135, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
;  APPLICANT:  Loring, Jeanne F.
;  APPLICANT:  Tingley, Debora W.
;  APPLICANT:  Edwards, Carla M.
;  TITLE OF INVENTION:  GENES EXPRESSED IN ALZHEIMER'S DISEASE
;  FILE REFERENCE:  PA-0024 US
;  CURRENT APPLICATION NUMBER: US/09/566,921
;  CURRENT FILING DATE:  2000-05-05
;  NUMBER OF SEQ ID NOS:  138
;  SOFTWARE:  PERL Program
; SEQ ID NO 135
;   LENGTH: 8044
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6682888 427813.14
US-09-566-921-135

  Query Match             99.8%;  Score 7780.6;  DB 4;  Length 8044;
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  Matches 7786;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

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Qy       1021 TCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGA 1080
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Db      3421 CCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGG 3480

Qy      3481 CAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTAT 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3481 CAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTAT 3540

Qy      3541 TCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCC 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3541 TCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCC 3600

Qy      3601 AAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGT 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3601 AAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGT 3660

Qy      3661 GACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTA 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3661 GACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTA 3720

Qy      3721 CACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGT 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3721 CACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGT 3780

Qy      3781 GACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCT 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3781 GACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCT 3840

Qy      3841 CACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAAC 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3841 CACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAAC 3900

Qy      3901 CCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTC 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3901 CCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTC 3960

Qy      3961 CTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAA 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3961 CTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAA 4020

Qy      4021 GGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCAC 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4021 GGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCAC 4080

Qy      4081 TGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCC 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4081 TGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCC 4140

Qy      4141 ATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGT 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 ATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGT 4200

Qy      4201 TGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGG 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 TGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGG 4260

Qy      4261 TACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAG 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4261 TACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAG 4320

Qy      4321 AGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGC 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4321 AGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGC 4380

Qy      4381 CAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCG 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4381 CAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCG 4440

Qy      4441 CCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAA 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4441 CCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAA 4500

Qy      4501 TTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4501 TTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCT 4560

Qy      4561 TAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCC 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4561 TAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCC 4620

Qy      4621 GAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4621 GAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCC 4680

Qy      4681 TGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGT 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4681 TGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGT 4740
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Qy      4741 CCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGG 4800
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Db      4741 CCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGG 4800

Qy      4801 AGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAG 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4801 AGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAG 4860

Qy      4861 CAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGAC 4920
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Db      4861 CAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGAC 4920

Qy      4921 CGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGG 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4921 CGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGG 4980

Qy      4981 TTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGG 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4981 TTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGG 5040

Qy      5041 TCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAG 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5041 TCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAG 5100

Qy      5101 TGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAA 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5101 TGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAA 5160

Qy      5161 CATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGC 5220
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Db      5161 CATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGC 5220

Qy      5221 TTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGA 5280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5221 TTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGA 5280

Qy      5281 TGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGG 5340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5281 TGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGG 5340

Qy      5341 CCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAG 5400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5341 CCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAG 5400

Qy      5401 CCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCAC 5460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5401 CCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCAC 5460

Qy      5461 TCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGG 5520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5461 TCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGG 5520

Qy      5521 ATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGC 5580
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Db      5521 ATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGC 5580

Qy      5581 TCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAG 5640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5581 TCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAG 5640

Qy      5641 TGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTGTCACCACTCT 5700
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db      5641 TGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGTTGTCACCACTCT 5700

Qy      5701 GGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCAC 5760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5701 GGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCAC 5760

Qy      5761 CATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGATGCCGTTCCAGC 5820
             ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db      5761 CATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGC 5820

Qy      5821 CAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCAC 5880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5821 CAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCAC 5880

Qy      5881 TGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCG 5940
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5881 AGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCG 5940

Qy      5941 GAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTT 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5941 GAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTT 6000

Qy      6001 CCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTAC 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6001 CCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTAC 6060

Qy      6061 CGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCC 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6061 CGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCC 6120

Qy      6121 CCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAAT 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6121 CCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAAT 6180

Qy      6181 TTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGAC 6240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6181 TTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGAC 6240

Qy      6241 AGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTT 6300
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Db      6241 AGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTT 6300

Qy      6301 GGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGG 6360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6301 GGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGG 6360

Qy      6361 AAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGAT 6420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6361 AAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGAT 6420

Qy      6421 CTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCA 6480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6421 CTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCA 6480

Qy      6481 TAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTC 6540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6481 TAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTC 6540

Qy      6541 ATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTGTTGGCACTGA 6600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6541 ATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTGTTGGCACTGA 6600

Qy      6601 TGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTCTGACAGGCCT 6660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6601 TGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTCTGACAGGCCT 6660

Qy      6661 CACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAA 6720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6661 CACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAA 6720

Qy      6721 GGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTAC 6780
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Db      6721 GGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTAC 6780

Qy      6781 GGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGGAGATGAGTGGGA 6840
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Qy      6841 ACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCA 6900
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Db      6841 ACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCA 6900

Qy      6901 TTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGA 6960
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b          6901 TTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGA 6960

y          6961 GAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTCTTGGGAACGG 7020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          6961 GAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTCTTGGGAACGG 7020

y          7021 AAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGATGGGAAGACATA 7080
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b          7021 AAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGATGGGAAGACATA 7080

y          7081 CCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTT 7140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          7081 CCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTT 7140

y          7141 TGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGGTGAACCCAGTCC 7200
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b          7141 TGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGGTGAACCCAGTCC 7200

y          7201 CGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCATCAGAGAACAAA 7260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          7201 CGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCATCAGAGAACAAA 7260

y          7261 CACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGGCTGACAGAGA 7320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          7261 CACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGGCTGACAGAGA 7320

y          7321 AGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCTCTCTGCCAAG 7380
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b          7321 AGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCTCTCTGCCAAG 7380

y          7381 ATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTCTTTCTTTCTTAA 7440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          7381 ATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTCTTTCTTTCTTAA 7440

y          7441 GCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCTTCTCCAAGCATC 7500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          7441 GCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCTTCTCCAAGCATC 7500

y          7501 ACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATTGCCTGTTCTGCT 7560
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          7501 ACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATTGCCTGTTCTGCT 7560

y          7561 TCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATTTGGTTTGGGA 7620
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b          7561 TCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATTTGGTTTGGGA 7620

y          7621 TCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGATATGACCAAA 7680
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b          7621 TCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGATATGACCAAA 7680

y          7681 ATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGTCTGGCCCGCAAT 7740
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          7681 ATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGTCTGGCCCGCAAT 7740

y          7741 ACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCACAGTACT 7795
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          7741 ACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCACAGTACT 7795

RESULT 2
US-09-220-132-38
; Sequence 38, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
;  APPLICANT:  Shyjan, Andrew W.
;  TITLE OF INVENTION:  METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT
;  TITLE OF INVENTION:  OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCE
;  FILE REFERENCE:  07334-074001
;  CURRENT APPLICATION NUMBER: US/09/220,132
;  CURRENT FILING DATE:  1998-12-23
;  PRIOR APPLICATION NUMBER:  US 60/079,303
;  PRIOR FILING DATE:  1998-03-25
;  PRIOR APPLICATION NUMBER:  US 60/068,821
;  PRIOR FILING DATE:  1997-12-24
;  NUMBER OF SEQ ID NOS:  191
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 38
;   LENGTH: 7679
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-220-132-38

  Query Match             95.2%;  Score 7423;  DB 4;  Length 7679;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7432;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy          409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy          469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
                |||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db          121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy          529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

Qy          589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

Qy          649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy          709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy          769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480

Qy          829 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 540

Qy          889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy          949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

Qy         1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy         1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy         1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy         1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG 1248
                |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db          841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGTTGAAGACACAAGG 900
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Qy   1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
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Db    901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy   1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy   1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy   1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy   1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy   1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy   1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy   1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy   1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy   1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy   1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy   1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy   1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy   2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy   2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy   2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy   2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy   2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980
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Qy   2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy   2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy   2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

Qy   2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

Qy   2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy   2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

Qy   2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy   2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy   2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

Qy   2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

Qy   2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
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Db   2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

Qy   2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
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Db   2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

Qy   3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy   3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy   3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy   3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy   3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy   3349 CCGACTGACCGTGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   3001 CCGACTGACCGTGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy   3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
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          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   3061 TGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy   3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy   3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy   3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy   3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy   3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy   3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy   3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy   3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600

Qy   3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
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Db   3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy   4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy   4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy   4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy   4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy   4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy   4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
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Db   3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy   4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
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Db   4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy   4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
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Db   4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy   4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
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Db   4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy   4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
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Db   4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy   4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
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Db   4261 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4320

Qy   4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy   4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
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Db   4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy   4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy   4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
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Db   4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy   4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
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Db   4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

Qy   4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
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Db   4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

Qy   5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy   5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
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Db   4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800

Qy   5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy   5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy   5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

Qy   5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy   5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy   5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy   5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
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Db   5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy   5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280
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Qy          5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy          5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
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Db          5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy          5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
                 ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
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Qy          5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
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Qy          5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
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Qy          5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
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Qy          5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
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Db          5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy          6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy          6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
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Db          5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

Qy          6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
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Qy          6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
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Db          5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy          6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
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Db          5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy          6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
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Db          6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy          6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
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Db          6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy          6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
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Db          6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

Qy          6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
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Qy          6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
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Db          6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300

Qy          6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
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Db          6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360
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Qy          6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
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Db          6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

Qy          6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
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Qy          6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
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Db          6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

Qy          6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
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Db          6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

Qy          6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
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Db          6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

Qy          7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
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Db          6661 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 6720

Qy          7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
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Db          6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

Qy          7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
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Qy          7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
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Db          6841 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 6900

Qy          7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
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Db          6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960

Qy          7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

Qy          7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
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Db          7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080

Qy          7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

Qy          7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
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Db          7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

Qy          7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
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Db          7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260

Qy          7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
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Db          7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

Qy          7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy          7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
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Qy          7789 CAGTACT 7795
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Db        7441 CAGTACT 7447

RESULT 3
US-09-023-655-1289
 Sequence 1289, Application US/09023655
 Patent No. 6607879
  GENERAL INFORMATION:
    APPLICANT:  Cocks, Benjamin G.
    APPLICANT:  Susan G. Stuart
    APPLICANT:  Jeffrey J. Seilhamer
    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
    TITLE OF INVENTION:  EXPRESSION
    NUMBER OF SEQUENCES:  1508
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
      STREET:  3174 PORTER DRIVE
      CITY:  PALO ALTO
      STATE:  CALIFORNIA
      COUNTRY:  USA
      ZIP:  94304
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/09/023,655
      FILING DATE:  HEREWITH
      CLASSIFICATION:
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:
      FILING DATE:
      CLASSIFICATION:
    ATTORNEY/AGENT INFORMATION:
      NAME:  Zeller, Karen J.
      REGISTRATION NUMBER:  37,071
      REFERENCE/DOCKET NUMBER:  PA-0001 US
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  (650) 855-0555
      TELEFAX:  (650) 845-4166
  INFORMATION FOR SEQ ID NO:  1289:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  7680 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  single
      TOPOLOGY:  linear
    IMMEDIATE SOURCE:
      LIBRARY:  GENBANK
      CLONE:  g31396
US-09-023-655-1289

 Query Match            95.2%;  Score 7423;  DB 4;  Length 7680;
 Best Local Similarity  99.8%;  Pred. No. 0;
 Matches 7432;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy        349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy        409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy        469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
              |||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy        529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
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Qy        589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
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Qy        649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
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Db        301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy        709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
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Db        361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy        769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
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Qy        829 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 540

Qy        889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
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Qy        949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

Qy       1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
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Db        661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy       1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
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Db        721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy       1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy       1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGATGCAGTGGCTGAAGACACAAGG 1248
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGATGCAGTGGTTGAAGACACAAGG 900

Qy       1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
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Db        901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy       1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
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Db        961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy       1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy       1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy       1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
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Db       1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy       1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
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Db       1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy       1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
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Db       1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy       1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
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Qy        1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy        1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
               |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy        1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
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Db        1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy        1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
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Db        1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy        1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy        2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy        2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy        2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy        2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy        2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy        2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy        2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy        2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

Qy        2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

Qy        2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy        2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

Qy        2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy        2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy        2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

Qy        2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

Qy        2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

Qy        3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy        3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy        3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy        3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy        3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy        3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
               ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy        3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
               |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        3061 TGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy        3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy        3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
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Db        3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy        3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy        3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy        3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy        3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
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Db        3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy        3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540
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Qy       3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
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Qy       3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
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Qy       4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy       4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy       4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy       4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy       4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy       4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy       4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
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Db       4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy       4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy       4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
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Qy       4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
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Db       4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy       4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy       4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy       4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
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Db       4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy       4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

Qy       4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy       5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
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Qy       5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
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Db       4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy       5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy       5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
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Db       4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

Qy       5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
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Db       4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy       5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
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Qy       5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
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Db       5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy       5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
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Qy       5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
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Db       5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy       5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy       5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy       5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
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Qy       5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
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Qy       5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
              |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
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Qy       5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
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Qy       5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
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Db       5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy       6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
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Db       5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy       6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
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Db       5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

Qy       6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
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Db       5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

Qy       6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy       6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy       6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy       6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
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Db       6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy       6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
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Qy       6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
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Db       6181 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

Qy       6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
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Db       6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300

Qy       6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360

Qy       6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

Qy       6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db       6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

Qy       6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

Qy       6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

Qy       6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

Qy       7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6661 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 6720

Qy       7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

Qy       7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6781 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840

Qy       7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6841 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 6900

Qy       7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960

Qy       7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

Qy       7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080

Qy       7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

Qy       7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

Qy       7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260

Qy       7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

Qy       7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy       7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440

Qy       7789 CAGTACT 7795
              |||||||
Db       7441 CAGTACT 7447
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RESULT 4
PCT-US95-09819-6
; Sequence 6, Application PC/TUS9509819
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNA
;    TITLE OF INVENTION:  CODING THEREFOR AND USES THEREOF
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/09819
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/283,857
;      FILING DATE:  01-AUG-1994
```

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    ATTORNEY/AGENT INFORMATION:
      NAME:  BROWDY, Roger L.
      REGISTRATION NUMBER:  25,618
      REFERENCE/DOCKET NUMBER:  GOLD=1A PCT
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  202-628-5197
      TELEFAX:  202-737-3528
      TELEX:  248633
  INFORMATION FOR SEQ ID NO:  6:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  7680 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  single
      TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA
CT-US95-09819-6

 Query Match             95.2%;  Score 7423;  DB 5;  Length 7680;
 Best Local Similarity   99.8%;  Pred. No. 0;
 Matches 7432;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

y         349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

y         409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

y         469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
              |||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
b         121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

y         529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

y         589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

y         649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

y         709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

y         769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480

y         829 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         481 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 540

y         889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

y         949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

y        1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

y        1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy       1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy       1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG 1248
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db        841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGTTGAAGACACAAGG 900

Qy       1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy       1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy       1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy       1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy       1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy       1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy       1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy       1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy       1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy       1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db       1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy       1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy       1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy       1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy       2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy       2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy       2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy       2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy       2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy       2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy       2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy       2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

Qy       2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

Qy       2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy       2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

Qy       2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy       2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy       2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

Qy       2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

Qy       2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

Qy       2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

Qy       3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy       3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy       3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy       3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy       3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy       3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy       3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy       3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy       3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db       3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy       3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy       3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy       3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy       3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy       3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy       3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600

Qy       3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy       4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy       4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy       4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy       4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy       4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy       4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy       4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080
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```
Qy    4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy    4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy    4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy    4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4261 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4320

Qy    4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy    4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy    4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy    4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy    4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

Qy    4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

Qy    5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy    5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800

Qy    5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy    5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy    5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

Qy    5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy    5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy    5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy    5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy    5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy    5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy    5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy    5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
           ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db    5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy    5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5461 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5520

Qy    5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
           |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db    5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

Qy    5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

Qy    5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy    6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy    6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

Qy    6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

Qy    6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy    6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy    6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy    6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy    6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

Qy    6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6181 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

Qy    6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300

Qy        6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360

Qy        6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

Qy        6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
               |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db        6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

Qy        6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

Qy        6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
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Db        6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

Qy        6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

Qy        7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6661 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 6720

Qy        7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

Qy        7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6781 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840

Qy        7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6841 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 6900

Qy        7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960

Qy        7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

Qy        7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080

Qy        7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

Qy        7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

Qy        7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260

Qy        7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

Qy        7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy        7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440

Qy        7789 CAGTACT 7795
               |||||||
Db        7441 CAGTACT 7447


RESULT 5
US-08-259-569-16
; Sequence 16, Application US/08259569
; Patent No. 5679320
;  GENERAL INFORMATION:
;    APPLICANT:  Vogel, Tikva
;    APPLICANT:  Levanon, Avigdor
;    APPLICANT:  Werber, Moshe
;    APPLICANT:  Guy, Rachel
;    APPLICANT:  Panet, Amos
;    APPLICANT:  Hartman, Jacob
;    APPLICANT:  Shaked, Hadassa
;    TITLE OF INVENTION:  FIBRIN BINDING DOMAIN POLYPEPTIDES AND
;    TITLE OF INVENTION:  USES AND METHODS OF PRODUCING SAME
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/259,569
;      FILING DATE:
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 703,842
;      FILING DATE:  21-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  25775-D/JPW/EAB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-977-9550
;      TELEFAX:  212-664-0525
;      TELEX:  422523 COOP UI
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7705 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  5..7681
US-08-259-569-16

  Query Match             95.2%;  Score 7418.2;  DB 1;  Length 7705;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7429;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy         349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy      409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy      469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
            |||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db      121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy      529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

Qy      589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

Qy      649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy      709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy      769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480

Qy      829 TGATCATGCTGCTGGACTTCCTATGTGGTCGGAGAAACGTGGAGAAGCCCTACCAAGG 888
            |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db      481 TGATCATGCTGCTGGACTCCCTATGTGGTCGGAGAAACGTGGAGAAGCCCTACCAAGG 540

Qy      889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy      949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
            |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db      601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTTGAGACACCTGGAG 660

Qy     1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy     1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy     1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy     1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG 1248
            |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db      841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGTTGAAGACACAAGG 900

Qy     1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy     1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
            ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy     1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
            ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db     1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy     1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy     1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy     1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
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Db     1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy     1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy     1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy     1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
            |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db     1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy     1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
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Db     1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy     1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
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Db     1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy     1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy     2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy     2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy     2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy     2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
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Db     1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy     2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy     2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy     2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
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Db     2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy     2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
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Qy     2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220
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Qy       2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy       2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy       2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy       2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
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Db       2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

Qy       2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
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Qy       2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
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Qy       3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
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Qy       3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
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Db       2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy       3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
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Qy       3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
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Qy       3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
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Qy       3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
              ||||| ||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TGTCTTCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy       3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
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Qy       3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
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Db       3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy       3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
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Qy       3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
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Qy       3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
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Db       3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy       3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
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Qy       4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
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Qy       4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
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Db       3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy       4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
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Qy       4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
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Qy       4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
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Qy       4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
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Qy       4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
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Qy       4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
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Db       4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

Qy       4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

Qy       5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy       5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800

Qy       5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy       5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy       5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

Qy       5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy       5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy       5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy       5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy       5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy       5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy       5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy       5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy       5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5461 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5520
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Qy       5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
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Db       5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

Qy       5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
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Db       5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

Qy       5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy       6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy       6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

Qy       6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

Qy       6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy       6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy       6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy       6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
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Db       6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy       6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
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Db       6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

Qy       6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6181 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

Qy       6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
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Db       6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300

Qy       6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360

Qy       6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

Qy       6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db       6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

Qy       6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

Qy       6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600
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Qy        6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
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Db        6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

Qy        7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
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Db        6661 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 6720

Qy        7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

Qy        7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
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Db        6781 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840

Qy        7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
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Db        6841 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 6900

Qy        7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960

Qy        7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

Qy        7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080

Qy        7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

Qy        7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
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Db        7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

Qy        7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
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Db        7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260

Qy        7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
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Db        7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

Qy        7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy        7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
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Qy        7789 CAGTACT 7795
               |||||||
Db        7441 CAGTACT 7447

RESULT 6
US-08-826-885-16
; Sequence 16, Application US/08826885
; Patent No. 5869616
;  GENERAL INFORMATION:
;    APPLICANT:  Vogel, Tikva
;    APPLICANT:  Levanon, Avigdor
;    APPLICANT:  Werber, Moshe
;    APPLICANT:  Guy, Rachel
;    APPLICANT:  Panet, Amos
;    APPLICANT:  Hartman, Jacob
;    APPLICANT:  Shaked, Hadassa
;    TITLE OF INVENTION:  FIBRIN BINDING DOMAIN POLYPEPTIDES AND
;    TITLE OF INVENTION:  USES AND METHODS OF PRODUCING SAME
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/826,885
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/703,842
;      FILING DATE:  21-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  25775-D/JPW/EAB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-977-9550
;      TELEFAX:  212-664-0525
;      TELEX:  422523 COOP UI
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7705 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  5..7681
US-08-826-885-16

  Query Match             95.2%;  Score 7418.2;  DB 2;  Length 7705;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7429;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy         349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy         409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy         469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
               |||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy         529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
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Qy         589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
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Qy         649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy         709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy   769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
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Db   421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480

Qy   829 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
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Db   481 TGATCATGCTGCTGGGACTCCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 540

Qy   889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy   949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
         |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTTGAGACACCTGGAG 660

Qy  1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy  1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy  1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy  1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGATGCAGTGGCTGAAGACACAAGG 1248
         ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGATGCAGTGGTTGAAGACACAAGG 900

Qy  1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy  1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
         ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy  1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
         ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db  1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy  1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy  1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
         ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy  1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
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Db  1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy  1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy  1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy  1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy  1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
         |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db  1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy  1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy  1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy  1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy  2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy  2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy  2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy  2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy  2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy  2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy  2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy  2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

Qy  2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

Qy  2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy  2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

Qy  2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy  2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy  2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

Qy  2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580
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Qy        2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

Qy        2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy        3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy        3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy        3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy        3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy        3349 CCGACTGACCGTGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
               ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        3001 CCGACTGACCGTGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy        3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
               ||||| ||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        3061 TGTCTTCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy        3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy        3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
               |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db        3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy        3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy        3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy        3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy        3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy        3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy        3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
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Qy        3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy        4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy        4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy        4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy        4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy        4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy        4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy        4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy        4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy        4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy        4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy        4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
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Db        4261 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4320

Qy        4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy        4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy        4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy        4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy        4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

Qy        5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy        5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800

Qy   5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy   5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy   5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
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Db   4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

Qy   5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
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Db   4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy   5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy   5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy   5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
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Db   5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy   5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy   5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy   5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy   5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
          ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy   5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
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Qy   5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
          |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
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Qy   5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

Qy   5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy   6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy   6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
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Qy   6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

Qy   6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy   6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
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Db   5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy   6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy   6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy   6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

Qy   6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6181 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

Qy   6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300

Qy   6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360

Qy   6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

Qy   6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
          |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

Qy   6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

Qy   6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

Qy   6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

Qy   7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6661 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 6720

Qy   7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

Qy   7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6781 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840

Qy   7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6841 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 6900

Qy   7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960
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Qy       7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

Qy       7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080

Qy       7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

Qy       7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

Qy       7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260

Qy       7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

Qy       7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy       7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440

Qy       7789 CAGTACT 7795
              |||||||
Db       7441 CAGTACT 7447


RESULT 7
5455158-2
;Patent No. 5455158
;    APPLICANT: VOGEL, TIKVA;LEVANON, AVIGDOR;WERBER, MOSHE M.;
;GUY, RACHEL;PANET, AMOS
;    TITLE OF INVENTION: FIBRIN BINDING DOMAIN POLYPEPTIDES AND
;USES AND METHODS OF PRODUCING SAME
;    NUMBER OF SEQUENCES: 20
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/58,241
;      FILING DATE: 04-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 526,397
;      FILING DATE: 21-MAY-1990
;      APPLICATION NUMBER: 345,952
;      FILING DATE: 28-APR-1989
;      APPLICATION NUMBER: 291,951
;      FILING DATE: 29-DEC-1988
;SEQ ID NO:2:
;      LENGTH: 7705
5455158-2

  Query Match             95.1%;  Score 7413.4;  DB 6;  Length 7705;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 7426;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy        349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy        409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGAGCG 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGAGCG 120

Qy        469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
              |||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy        529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

Qy'       589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

Qy        649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy        709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy        769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480

Qy        829 TGATCATGCTGCTGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        481 TGATCATGCTGCTGGACTCCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 540

Qy        889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy        949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db        601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTTGAGACACCTGGAG 660

Qy       1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy       1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy       1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy       1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG 1248
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGTTGAAGACACAAGG 900

Qy       1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy       1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy       1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy       1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy       1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy       1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy   1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy   1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy   1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy   1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy   1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy   1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy   1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCACTG 1680

Qy   2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy   2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy   2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy   2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy   2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy   2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy   2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy   2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

Qy   2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

Qy   2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy   2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340
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Qy   2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy   2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy   2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

Qy   2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

Qy   2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
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Db   2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

Qy   2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

Qy   3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy   3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy   3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy   3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy   3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy   3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy   3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
          ||||| ||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   3061 TGTCTTCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy   3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy   3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
          ||||||||||||||||||||||||||||||||||||||||| |||||| |||||||||||
Db   3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGAGCACCATCGTGATCACATG 3240

Qy   3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy   3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy   3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420
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Qy   3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
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Db   3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy   3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy   3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600

Qy   3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy   4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy   4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy   4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy   4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
          |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCTGTGGTCTTAACAAA 3900

Qy   4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy   4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy   4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy   4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy   4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy   4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy   4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4320

Qy   4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy   4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy   4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy   4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy   4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

Qy   4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

Qy   5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy   5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800

Qy   5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy   5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
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Db   4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy   5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

Qy   5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
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Db   4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy   5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy   5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy   5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy   5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy   5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy   5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy   5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
          ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy   5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5520

Qy   5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
          |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db   5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

Qy   5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

y           5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

y           6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

y           6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

y           6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

y           6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

y           6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

y           6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

y           6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

y           6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

y           6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           6181 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

y           6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300

y           6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360

y           6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

y           6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
                 |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
b           6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

y           6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

y           6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

y           6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

y           7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           6661 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 6720
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Qy          7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
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Db          6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

Qy          7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6781 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840

Qy          7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6841 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 6900

Qy          7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960

Qy          7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

Qy          7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080

Qy          7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

Qy          7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

Qy          7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260

Qy          7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

Qy          7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy          7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440

Qy          7789 CAGTACT 7795
                 |||||||
Db          7441 CAGTACT 7447


RESULT 8
US-08-551-356-1
; Sequence 1, Application US/08551356
; Patent No. 5830700
;  GENERAL INFORMATION:
;    APPLICANT:  Irani, Meher
;    TITLE OF INVENTION:  HYBRID CROSS-LINKING PROTEINS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  4225 Roosevelt Way, N.E.
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/551,356
;     FILING DATE:
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/349,762
;     FILING DATE:
;     APPLICATION NUMBER:  US/07/998,271
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Holly, Julie A
;     REGISTRATION NUMBER:  33-246
;     REFERENCE/DOCKET NUMBER:  92-26
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  206-547-8080 ext 322
;     TELEFAX:  206-548-2329
; INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  7803 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  6..7346
US-08-551-356-1

  Query Match             92.7%;  Score 7223;  DB 2;  Length 7803;
  Best Local Similarity   96.3%;  Pred. No. 0;
  Matches 7515;  Conservative    0;  Mismatches   15;  Indels  273;  Gaps    1;

Qy        264 TCAACATGCTTAGGGGTCCGGGGCCCGGGCTGCTGCTGCTGGCCGTCCTGTGCCTGGGGA 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCAACATGCTTAGGGGTCCGGGGCCCGGGCTGCTGCTGCTGGCCGTCCTGTGCCTGGGGA 60

Qy        324 CAGCGGTGCCCTCCACGGGAGCCTCGAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGC 383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGCGGTGCCCTCCACGGGAGCCTCGAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGC 120

Qy        384 CCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCGGTTGTTATGACAATGGAAAACACT 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCGGTTGTTATGACAATGGAAAACACT 180

Qy        444 ATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGCAATGCGTTGGTTTGTACTTGTT 503
              ||||||||||||||||||||||||||||||||||||| |||| |||||||||||||||||
Db        181 ATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGTAATGTGTTGGTTTGTACTTGTT 240

Qy        504 ATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTG 563
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTG 300

Qy        564 ACAAGTACACTGGGAACACTTACCGAGTGGGTGACACTTATGAGCGTCCTAAAGACTCCA 623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACAAGTACACTGGGAACACTTACCGAGTGGGTGACACTTATGAGCGTCCTAAAGACTCCA 360

Qy        624 TGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAA 683
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAA 420

Qy        684 ACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGGTGACACCTGGAGGAGACCACATG 743
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGGTGACACCTGGAGGAGACCACATG 480

Qy        744 AGACTGGTGGTTACATGTTAGAGTGTGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCT 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGACTGGTGGTTACATGTTAGAGTGTGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCT 540

Qy        804 GCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGTCGGAG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGTCGGAG 600

Qy        864 AAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAG 923
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAG 660

Qy        924 GCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACAT 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACAT 720

Qy        984 CCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCA 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCA 780

Qy       1044 TCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCA 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCA 840

Qy       1104 CATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTC 1163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTC 900

Qy       1164 ACCCCCAGCCTCCTCCCTATGGCCACTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGG 1223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ACCCCCAGCCTCCTCCCTATGGCCACTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGG 960

Qy       1224 GGATGCAGTGGCTGAAGACACAAGGAAATAAGCAAATGCTTTGCACGTGCCTGGGCAACG 1283
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGATGCAGTGGTTGAAGACACAAGGAAATAAGCAAATGCTTTGCACGTGCCTGGGCAACG 1020

Qy       1284 GAGTCAGCTGCCAAGAGACAGCTGTAACCCAGACTTACGGTGGCAACTCAAATGGAGAGC 1343
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db       1021 GAGTCAGCTGCCAAGAGACAGCTGTAACCCAGACTTACGGTGGCAACTTAAATGGAGAGC 1080

Qy       1344 CATGTGTCTTACCATTCACCTACAATGGCAGGACGTTCTACTCCTGCACCACAGAAGGGC 1403
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       1081 CATGTGTCTTACCATTCACCTACAATGGCAGGACGTTCTACTCCTGCACCACGGAAGGGC 1140

Qy       1404 GACAGGACGGACATCTTTGGTGCAGCACAACTTCGAATTATGAGCAGGACCAGAAATACT 1463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GACAGGACGGACATCTTTGGTGCAGCACAACTTCGAATTATGAGCAGGACCAGAAATACT 1200

Qy       1464 CTTTCTGCACAGACCACACTGTTTTGGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCT 1523
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db       1201 CTTTCTGCACAGACCACACTGTTTTGGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCT 1260

Qy       1524 TGTGCCACTTCCCCTTCCTATACAACAACCACAATTACACTGATTGCACTTCTGAGGGCA 1583
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGTGCCACTTCCCCTTCCTATACAACAACCACAATTACACTGATTGCACTTCTGAGGGCA 1320

Qy       1584 GAAGAGACAACATGAAGTGGTGTGGGACCACACAGAACTATGATGCCGACCAGAAGTTTG 1643
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAAGAGACAACATGAAGTGGTGTGGGACCACACAGAACTATGATGCCGACCAGAAGTTTG 1380

Qy       1644 GGTTCTGCCCCATGGCTGCCCACGAGGAAATCTGCACAACCAATGAAGGGGTCATGTACC 1703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGTTCTGCCCCATGGCTGCCCACGAGGAAATCTGCACAACCAATGAAGGGGTCATGTACC 1440

Qy       1704 GCATTGGAGATCAGTGGGATAAGCAGCATGACATGGGTCACATGATGAGGTGCACGTGTG 1763
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GCATTGGAGATCAGTGGGATAAGCAGCATGACATGGGTCACATGATGAGGTGCACGTGTG 1500

Qy       1764 TTGGGAATGGTCGTGGGGAATGGACATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCA 1823
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1501 TTGGGAATGGTCGTGGGGAATGGACATGCATTGCCTACTCGCAACTTCGAGATCAGTGCA 1560

Qy       1824 TTGTTGATGACATCACTTACAATGTGAACGACACATTCCACAAGCGTCATGAAGAGGGGC 1883
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TTGTTGATGACATCACTTACAATGTGAACGACACATTCCACAAGCGTCATGAAGAGGGGC 1620

Qy       1884 ACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCG 1943
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Db       1621 ACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCG 1680

Qy       1944 ACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCAAATTGGAGATTCATGGGAGAAGT 2003
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 ACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCAAATTGGAGATTCATGGGAGAAGT 1740

Qy      2004 ATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGCCGTGGCATTGGGGAGTGGCATT 2063
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 ATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGCCGTGGCATTGGGGAGTGGCATT 1800

Qy      2064 GCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGA 2123
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 GCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGA 1860

Qy      2124 CTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAATGCACCACAGCCATCTCACATTT 2183
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 CTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAATGCACCACAGCCATCTCACATTT 1920

Qy      2184 CCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCA 2243
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 CCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCA 1980

Qy      2244 TACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGG 2303
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 TACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGG 2040

Qy      2304 GCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAAGTGACTCGCTTTGACTTCACCA 2363
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 GCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAAGTGACTCGCTTTGACTTCACCA 2100

Qy      2364 CCACCAGCACCAGCACACCTGTGACCAGCAACACCGTGACAGGAGAGACGACTCCCTTTT 2423
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 CCACCAGCACCAGCACACCTGTGACCAGCAACACCGTGACAGGAGAGACGACTCCCTTTT 2160

Qy      2424 CTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCT 2483
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 CTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCT 2220

Qy      2484 CCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGG 2543
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 CCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGG 2280

Qy      2544 AGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACAGCCACTTCTGTGAACATCCCTG 2603
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 AGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACAGCCACTTCTGTGAACATCCCTG 2340

Qy      2604 ACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTATCAGATATCTGAGGATGGGGAGC 2663
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 ACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTATCAGATATCTGAGGATGGGGAGC 2400

Qy      2664 AGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCCTGATGCCCCTCCTGACCCGACTG 2723
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 AGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCCTGATGCCCCTCCTGACCCGACTG 2460

Qy      2724 TGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCA 2783
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461 TGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCA 2520

Qy      2784 CAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTC 2843
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521 CAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTC 2580

Qy      2844 CTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAACCTGGTGTTCAGTATAACATCA 2903
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Db      2581 CTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAACCTGGTGTTCAGTATAACATCA 2640

Qy      2904 CTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCTGTTGTCATTCAACAAGAAACCA 2963
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Db      2641 CTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCTGTTGTCATTCAACAAGAAACCA 2700

Qy      2964 CTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGA 3023
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Db      2701 CTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGA 2760

Qy      3024 CAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAGAGTGCAGTGACCGGCTACCGTG 3083
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761 CAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAGAGTGCAGTGACCGGCTACCGTG 2820

Qy      3084 TGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGA 3143
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821 TGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGA 2880

Qy      3144 ACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTG 3203
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Db      2881 ACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTG 2940

Qy      3204 CAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCTCAACAGACAACCAAACTGGATG 3263
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2941 CAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCTCAACAGACAACCAAACTGGATG 3000

Qy      3264 CTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCTACTGTCCTGGTGAGATGGACTC 3323
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3001 CTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCTACTGTCCTGGTGAGATGGACTC 3060

Qy      3324 CACCTCGGGCCCAGATAACAGGATACCGACTGACCGTGGGCCTTACCCGAAGAGGACAGC 3383
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db      3061 CACCTCGGGCCCAGATAACAGGATACCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGC 3120

Qy      3384 CCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTG 3443
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db      3121 CCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTG 3180

Qy      3444 CATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCA 3503
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3181 CATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCA 3240

Qy      3504 CTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATTCCACCTTACAACACCGAGGTGA 3563
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Db      3241 CTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATTCCACCTTACAACACCGAGGTGA 3300

Qy      3564 CTGAGACCACCATTGTGATCACATGGACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTG 3623
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Db      3301 CTGAGACCACCATCGTGATCACATGGACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTG 3360

Qy      3624 TACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTGACTTCAGACTCAGGAAGCATCG 3683
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Db      3361 TACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTGACTTCAGACTCAGGAAGCATCG 3420

Qy      3684 TTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTACACCATCCAAGTCCTGAGAGATG 3743
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Db      3421 TTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTACACCATCCAAGTCCTGAGAGATG 3480

Qy      3744 GACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTGACACCATTGTCTCCACCAACAA 3803
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Db      3481 GACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTGACACCATTGTCTCCACCAACAA 3540

Qy      3804 ACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCA 3863
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Db      3541 ACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCA 3600

Qy      3864 CCACCCCAGACATTACTGGTTATAGAATTACCACAACCCCTACAAACGGCCAGCAGGGAA 3923
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3601 CCACCCCAGACATTACTGGTTATAGAATTACCACAACCCCTACAAACGGCCAGCAGGGAA 3660

Qy      3924 ATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCCTGCACTTTTGATAACCTGAGTC 3983
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Db      3661 ATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCCTGCACTTTTGATAACCTGAGTC 3720

Qy      3984 CCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAGGATGACAAGGAAAGTGTCCCTA 4043
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Db      3721 CCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAGGATGACAAGGAAAGTGTCCCTA 3780

Qy      4044 TCTCTGATACCATCATCCCA---------------------------------------- 4063
             ||||||||||||||||||||
Db      3781 TCTCTGATACCATCATCCCAGAGGTGCCCCAACTCACTGACCTAAGCTTTGTTGATATAA 3840

Qy      4064 ------------------------------------------------------------ 4063

Db      3841 CCGATTCAAGCATCGGCCTGAGGTGGACCCCGCTAAACTCTTCCACCATTATTGGGTACC 3900
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Qy          4064 ------------------------------------------------------------ 4063

Db          3901 GCATCACAGTAGTTGCGGCAGGAGAAGGTATCCCTATTTTTGAAGATTTTGTGTACTCCT 3960

Qy          4064 ------------------------------------------------------------ 4063

Db          3961 CAGTAGGATACTACACAGTCACAGGGCTGGAGCCGGGCATTGACTATGATATCAGCGTTA 4020

Qy          4064 -----------------------------------------------------GCTGTTC 4070
                                                                      |||||||
Db          4021 TCACTCTCATTAATGGCGGCGAGAGTGCCCCTACTACACTGACACAACAAACGGCTGTTC 4080

Qy          4071 CTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGG 4130
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4081 CTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGG 4140

Qy          4131 CTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATG 4190
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Db          4141 CTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATG 4200

Qy          4191 AGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATC 4250
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Db          4201 AGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATC 4260

Qy          4251 TCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCA 4310
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Db          4261 TCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCA 4320

Qy          4311 CACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTG 4370
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Db          4321 CACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTG 4380

Qy          4371 ATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCT 4430
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4381 ATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCT 4440

Qy          4431 ACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCC 4490
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4441 ACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCC 4500

Qy          4491 ACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCA 4550
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4501 ACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCA 4560

Qy          4551 TCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTT 4610
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4561 TCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTT 4620

Qy          4611 CTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCT 4670
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Db          4621 CTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCT 4680

Qy          4671 GGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAA 4730
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Db          4681 GGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAA 4740

Qy          4731 ATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCC 4790
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4741 ATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCC 4800

Qy          4791 TTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCC 4850
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4801 TTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCC 4860

Qy          4851 CCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGA 4910
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4861 CCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGA 4920

Qy          4911 TGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCC 4970
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4921 TGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCC 4980

Qy          4971 CTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTA 5030
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4981 CTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTA 5040

Qy          5031 AAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGT 5090
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5041 AAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGT 5100

Qy          5091 ATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTG 5150
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5101 ATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTG 5160

Qy          5151 CAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCA 5210
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5161 CAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCA 5220

Qy          5211 TCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGA 5270
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5221 TCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGA 5280

Qy          5271 GCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAG 5330
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5281 GCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAG 5340

Qy          5331 AGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATG 5390
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5341 AGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATG 5400

Qy          5391 ATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACC 5450
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5401 ATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACC 5460

Qy          5451 TGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTC 5510
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5461 TGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTC 5520

Qy          5511 AGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAA 5570
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5521 AGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAA 5580

Qy          5571 TCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAAT 5630
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5581 TCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAAT 5640

Qy          5631 ATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTG 5690
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db          5641 ATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGTTG 5700

Qy          5691 TCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGA 5750
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5701 TCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGA 5760

Qy          5751 CCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGATG 5810
                 ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db          5761 CCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATG 5820

Qy          5811 CCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCT 5870
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5821 CCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCT 5880

Qy          5871 ACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATG 5930
                 |||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||
Db          5881 ACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATG 5940

Qy          5931 ACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCA 5990
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5941 ACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCA 6000

Qy          5991 ACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTG 6050
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6001 ACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTG 6060

Qy          6051 CCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGG 6110
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6061 CCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGG 6120

Qy        6111 TCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCG 6170
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6121 TCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCG 6180

Qy        6171 AATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAA 6230
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6181 AATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAA 6240

Qy        6231 GGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGAC 6290
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6241 GGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGAC 6300

Qy        6291 CAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGT 6350
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6301 CAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGT 6360

Qy        6351 ATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGC 6410
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6361 ATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGC 6420

Qy        6411 AACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCC 6470
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6421 AACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCC 6480

Qy        6471 CCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGA 6530
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6481 CCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGA 6540

Qy        6531 CAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTG 6590
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6541 CAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTG 6600

Qy        6591 TTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTC 6650
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6601 TTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTC 6660

Qy        6651 TGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGC 6710
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6661 TGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGC 6720

Qy        6711 AGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGA 6770
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6721 AGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGA 6780

Qy        6771 ACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGGAG 6830
               |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db        6781 ACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGGAG 6840

Qy        6831 ATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTG 6890
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6841 ATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTG 6900

Qy        6891 GAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTACA 6950
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6901 GAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTACA 6960

Qy        6951 AGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTC 7010
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6961 AGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTC 7020

Qy        7011 TTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGATG 7070
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7021 TTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGATG 7080

Qy        7071 GGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCT 7130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7081 GGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCT 7140

Qy        7131 GCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGGTG 7190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7141 GCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGGTG 7200

Qy        7191 AACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCATC 7250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7201 AACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCATC 7260

Qy        7251 AGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGG 7310
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7261 AGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGG 7320

Qy        7311 CTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCT 7370
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7321 CTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCT 7380

Qy        7371 CTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTCTT 7430
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7381 CTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTCTT 7440

Qy        7431 TCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCTTC 7490
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7441 TCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCTTC 7500

Qy        7491 TCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATTGC 7550
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7501 TCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATTGC 7560

Qy        7551 CTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATT 7610
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7561 CTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATT 7620

Qy        7611 TGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGA 7670
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7621 TGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGA 7680

Qy        7671 TATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGTCT 7730
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7681 TATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGTCT 7740

Qy        7731 GGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCACA 7790
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7741 GGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCACA 7800

Qy        7791 GTA 7793
               |||
Db        7801 GTA 7803


RESULT 9
PCT-US93-12687-1
; Sequence 1, Application PC/TUS9312687
;  GENERAL INFORMATION:
;    APPLICANT:  Irani, Meher H.
;    TITLE OF INVENTION:  HYBRID CROSS-LINKING PROTEINS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  4225 Roosevelt Way, N.E.
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/12687
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/998,271
;      FILING DATE:  31-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
```

```
;      NAME:  Parker, Gary E
;      REGISTRATION NUMBER:  31-648
;      REFERENCE/DOCKET NUMBER:  92-26PC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-547-8080 ext 322
;      TELEFAX:  206-548-2329
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7803 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  6..7346
PCT-US93-12687-1

  Query Match             92.7%;  Score 7223;  DB 5;  Length 7803;
  Best Local Similarity   96.3%;  Pred. No. 0;
  Matches 7515;  Conservative    0;  Mismatches   15;  Indels  273;  Gaps    1;

Qy        264 TCAACATGCTTAGGGGTCCGGGGCCCGGGCTGCTGCTGCTGGCCGTCCTGTGCCTGGGGA 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCAACATGCTTAGGGGTCCGGGGCCCGGGCTGCTGCTGCTGGCCGTCCTGTGCCTGGGGA 60

Qy        324 CAGCGGTGCCCTCCACGGGAGCCTCGAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGC 383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGCGGTGCCCTCCACGGGAGCCTCGAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGC 120

Qy        384 CCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCGGTTGTTATGACAATGGAAAACACT 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCGGTTGTTATGACAATGGAAAACACT 180

Qy        444 ATCAGATAAATCAACAGTGGAGCGGACCTACCTAGGCAATGCGTTGGTTTGTACTTGTT 503
              |||||||||||||||||||||||||||||||||||| |||| ||||||||||||||||||
Db        181 ATCAGATAAATCAACAGTGGAGCGGACCTACCTAGGTAATGTGTTGGTTTGTACTTGTT 240

Qy        504 ATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTG 563
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTG 300

Qy        564 ACAAGTACACTGGGAACACTTACCGAGTGGGTGACACTTATGAGCGTCCTAAAGACTCCA 623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACAAGTACACTGGGAACACTTACCGAGTGGGTGACACTTATGAGCGTCCTAAAGACTCCA 360

Qy        624 TGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAA 683
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAA 420

Qy        684 ACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGGTGACACCTGGAGGAGACCACATG 743
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGGTGACACCTGGAGGAGACCACATG 480

Qy        744 AGACTGGTGGTTACATGTTAGAGTGTGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCT 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGACTGGTGGTTACATGTTAGAGTGTGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCT 540

Qy        804 GCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGTCGGAG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGTCGGAG 600

Qy        864 AAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAG 923
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAG 660

Qy        924 GCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACAT 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAGGACAT 720

Qy        984 CCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCA 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCA 780
```

```
Qy       1044 TCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCA 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCA 840

Qy       1104 CATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTC 1163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTC 900

Qy       1164 ACCCCCAGCCTCCTCCCTATGGCCACTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGG 1223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ACCCCCAGCCTCCTCCCTATGGCCACTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGG 960

Qy       1224 GGATGCAGTGGCTGAAGACACAAGGAAATAAGCAAATGCTTTGCACGTGCCTGGGCAACG 1283
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGATGCAGTGGTTGAAGACACAAGGAAATAAGCAAATGCTTTGCACGTGCCTGGGCAACG 1020

Qy       1284 GAGTCAGCTGCCAAGAGACAGCTGTAACCCAGACTTACGGTGGCAACTCAAATGGAGAGC 1343
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db       1021 GAGTCAGCTGCCAAGAGACAGCTGTAACCCAGACTTACGGTGGCAACTTAAATGGAGAGC 1080

Qy       1344 CATGTGTCTTACCATTCACCTACAATGGCAGGACGTTCTACTCCTGCACCACAGAAGGGC 1403
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       1081 CATGTGTCTTACCATTCACCTACAATGGCAGGACGTTCTACTCCTGCACCACGGAAGGGC 1140

Qy       1404 GACAGGACGGACATCTTTGGTGCAGCACAACTTCGAATTATGAGCAGGACCAGAAATACT 1463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GACAGGACGGACATCTTTGGTGCAGCACAACTTCGAATTATGAGCAGGACCAGAAATACT 1200

Qy       1464 CTTTCTGCACAGACCACACTGTTTTGGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCT 1523
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db       1201 CTTTCTGCACAGACCACACTGTTTTGGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCT 1260

Qy       1524 TGTGCCACTTCCCCTTCCTATACAACAACCACAATTACACTGATTGCACTTCTGAGGGCA 1583
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGTGCCACTTCCCCTTCCTATACAACAACCACAATTACACTGATTGCACTTCTGAGGGCA 1320

Qy       1584 GAAGAGACAACATGAAGTGGTGTGGGACCACACAGAACTATGATGCCGACCAGAAGTTTG 1643
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAAGAGACAACATGAAGTGGTGTGGGACCACACAGAACTATGATGCCGACCAGAAGTTTG 1380

Qy       1644 GGTTCTGCCCCATGGCTGCCCACGAGGAAATCTGCACAACCAATGAAGGGGTCATGTACC 1703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGTTCTGCCCCATGGCTGCCCACGAGGAAATCTGCACAACCAATGAAGGGGTCATGTACC 1440

Qy       1704 GCATTGGAGATCAGTGGGATAAGCAGCATGACATGGGTCACATGATGAGGTGCACGTGTG 1763
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GCATTGGAGATCAGTGGGATAAGCAGCATGACATGGGTCACATGATGAGGTGCACGTGTG 1500

Qy       1764 TTGGGAATGGTCGTGGGGAATGGACATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCA 1823
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db       1501 TTGGGAATGGTCGTGGGGAATGGACATGCATTGCCTACTCGCAACTTCGAGATCAGTGCA 1560

Qy       1824 TTGTTGATGACATCACTTACAATGTGAACGACACATTCCACAAGCGTCATGAAGAGGGGC 1883
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TTGTTGATGACATCACTTACAATGTGAACGACACATTCCACAAGCGTCATGAAGAGGGGC 1620

Qy       1884 ACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCG 1943
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 ACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCG 1680

Qy       1944 ACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCAAATTGGAGATTCATGGGAGAAGT 2003
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCAAATTGGAGATTCATGGGAGAAGT 1740

Qy       2004 ATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGCCGTGGCATTGGGGAGTGGCATT 2063
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 ATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGCCGTGGCATTGGGGAGTGGCATT 1800

Qy       2064 GCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGA 2123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGA 1860

Qy       2124 CTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAATGCACCACAGCCATCTCACATTT 2183
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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 CTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAATGCACCACAGCCATCTCACATTT 1920

Qy  2184 CCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCA 2243
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 CCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCA 1980

Qy  2244 TACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGG 2303
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 TACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGG 2040

Qy  2304 GCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAAGTGACTCGCTTTGACTTCACCA 2363
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 GCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAAGTGACTCGCTTTGACTTCACCA 2100

Qy  2364 CCACCAGCACCAGCACACCTGTGACCAGCAACACCGTGACAGGAGAGACGACTCCCTTTT 2423
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 CCACCAGCACCAGCACACCTGTGACCAGCAACACCGTGACAGGAGAGACGACTCCCTTTT 2160

Qy  2424 CTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCT 2483
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 CTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCT 2220

Qy  2484 CCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGG 2543
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 CCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGG 2280

Qy  2544 AGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACAGCCACTTCTGTGAACATCCCTG 2603
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 AGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACAGCCACTTCTGTGAACATCCCTG 2340

Qy  2604 ACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTATCAGATATCTGAGGATGGGGAGC 2663
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 ACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTATCAGATATCTGAGGATGGGGAGC 2400

Qy  2664 AGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCCTGATGCCCCTCCTGACCCGACTG 2723
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 AGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCCTGATGCCCCTCCTGACCCGACTG 2460

Qy  2724 TGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCA 2783
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 TGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCA 2520

Qy  2784 CAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTC 2843
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 CAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTC 2580

Qy  2844 CTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAACCTGGTGTTCAGTATAACATCA 2903
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 CTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAACCTGGTGTTCAGTATAACATCA 2640

Qy  2904 CTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCTGTTGTCATTCAACAAGAAACCA 2963
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 CTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCTGTTGTCATTCAACAAGAAACCA 2700

Qy  2964 CTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGA 3023
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 CTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGA 2760

Qy  3024 CAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAGAGTGCAGTGACCGGCTACCGTG 3083
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 CAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAGAGTGCAGTGACCGGCTACCGTG 2820

Qy  3084 TGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGA 3143
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821 TGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGA 2880

Qy  3144 ACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTG 3203
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 ACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTG 2940

Qy  3204 CAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCTCAACAGACAACCAAACTGGATG 3263
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  2941 CAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCTCAACAGACAACCAAACTGGATG 3000

Qy  3264 CTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCTACTGTCCTGGTGAGATGGACTC 3323
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 CTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCTACTGTCCTGGTGAGATGGACTC 3060

Qy  3324 CACCTCGGGCCCAGATAACAGGATACCGACTGACCGTGGGCCTTACCCGAAGAGGACAGC 3383
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db  3061 CACCTCGGGCCCAGATAACAGGATACCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGC 3120

Qy  3384 CCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTG 3443
         |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db  3121 CCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTG 3180

Qy  3444 CATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCA 3503
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 CATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCA 3240

Qy  3504 CTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATTCCACCTTACAACACCGAGGTGA 3563
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 CTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATTCCACCTTACAACACCGAGGTGA 3300

Qy  3564 CTGAGACCACCATTGTGATCACATGGACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTG 3623
         ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 CTGAGACCACCATCGTGATCACATGGACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTG 3360

Qy  3624 TACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTGACTTCAGACTCAGGAAGCATCG 3683
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 TACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTGACTTCAGACTCAGGAAGCATCG 3420

Qy  3684 TTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTACACCATCCAAGTCCTGAGAGATG 3743
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 TTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTACACCATCCAAGTCCTGAGAGATG 3480

Qy  3744 GACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTGACACCATTGTCTCCACCAACAA 3803
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 GACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTGACACCATTGTCTCCACCAACAA 3540

Qy  3804 ACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCA 3863
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 ACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCA 3600

Qy  3864 CCACCCCAGACATTACTGGTTATAGAATTACCACAACCCCTACAAACGGCCAGCAGGGAA 3923
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 CCACCCCAGACATTACTGGTTATAGAATTACCACAACCCCTACAAACGGCCAGCAGGGAA 3660

Qy  3924 ATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCCTGCACTTTTGATAACCTGAGTC 3983
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 ATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCCTGCACTTTTGATAACCTGAGTC 3720

Qy  3984 CCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAGGATGACAAGGAAAGTGTCCCTA 4043
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 CCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAGGATGACAAGGAAAGTGTCCCTA 3780

Qy  4044 TCTCTGATACCATCATCCCA---------------------------------------- 4063
         ||||||||||||||||||||
Db  3781 TCTCTGATACCATCATCCCAGAGGTGCCCCAACTCACTGACCTAAGCTTTGTTGATATAA 3840

Qy  4064 ------------------------------------------------------------ 4063

Db  3841 CCGATTCAAGCATCGGCCTGAGGTGGACCCCGCTAAACTCTTCCACCATTATTGGGTACC 3900

Qy  4064 ------------------------------------------------------------ 4063

Db  3901 GCATCACAGTAGTTGCGGCAGGAGAAGGTATCCCTATTTTTGAAGATTTTGTGTACTCCT 3960

Qy  4064 ------------------------------------------------------------ 4063

Db  3961 CAGTAGGATACTACACAGTCACAGGGCTGGAGCCGGGCATTGACTATGATATCAGCGTTA 4020

Qy  4064 -----------------------------------------------------GCTGTTC 4070
                                                              |||||||
Db  4021 TCACTCTCATTAATGGCGGCGAGAGTGCCCCTACTACACTGACACAACAAACGGCTGTTC 4080
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Qy       4071 CTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGG 4130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 CTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGG 4140

Qy       4131 CTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATG 4190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 CTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATG 4200

Qy       4191 AGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATC 4250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 AGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATC 4260

Qy       4251 TCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCA 4310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 TCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCA 4320

Qy       4311 CACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTG 4370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 CACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTG 4380

Qy       4371 ATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCT 4430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 ATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCT 4440

Qy       4431 ACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCC 4490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 ACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCC 4500

Qy       4491 ACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCA 4550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 ACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCA 4560

Qy       4551 TCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTT 4610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 TCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTT 4620

Qy       4611 CTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCT 4670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCT 4680

Qy       4671 GGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAA 4730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 GGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAA 4740

Qy       4731 ATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCC 4790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 ATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCC 4800

Qy       4791 TTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCC 4850
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 TTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCC 4860

Qy       4851 CCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGA 4910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 CCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGA 4920

Qy       4911 TGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCC 4970
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 TGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCC 4980

Qy       4971 CTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTA 5030
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 CTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTA 5040

Qy       5031 AAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGT 5090
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 AAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGT 5100

Qy       5091 ATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTG 5150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 ATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTG 5160

Qy       5151 CAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCA 5210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 CAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCA 5220

Qy       5211 TCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGA 5270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 TCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGA 5280

Qy       5271 GCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAG 5330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5281 GCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAG 5340

Qy       5331 AGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATG 5390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5341 AGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATG 5400

Qy       5391 ATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACC 5450
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5401 ATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACC 5460

Qy       5451 TGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTC 5510
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5461 TGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTC 5520

Qy       5511 AGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAA 5570
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5521 AGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAA 5580

Qy       5571 TCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAAT 5630
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5581 TCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAAT 5640

Qy       5631 ATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTG 5690
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       5641 ATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGTTG 5700

Qy       5691 TCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGA 5750
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5701 TCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGA 5760

Qy       5751 CCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGATG 5810
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       5761 CCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATG 5820

Qy       5811 CCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCT 5870
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5821 CCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCT 5880

Qy       5871 ACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATG 5930
              |||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 ACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATG 5940

Qy       5931 ACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCA 5990
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 ACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCA 6000

Qy       5991 ACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTG 6050
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 ACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTG 6060

Qy       6051 CCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGG 6110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 CCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGG 6120

Qy       6111 TCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCG 6170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 TCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCG 6180

Qy       6171 AATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAA 6230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6181 AATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAA 6240

Qy       6231 GGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGAC 6290
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          6241 GGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGAC 6300

y          6291 CAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGT 6350
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          6301 CAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGT 6360

y          6351 ATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGC 6410
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          6361 ATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGC 6420

y          6411 AACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCC 6470
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          6421 AACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCC 6480

y          6471 CCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGA 6530
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          6481 CCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGA 6540

y          6531 CAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTG 6590
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          6541 CAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTG 6600

y          6591 TTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTC 6650
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          6601 TTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTC 6660

y          6651 TGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGC 6710
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          6661 TGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGC 6720

y          6711 AGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGA 6770
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          6721 AGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGA 6780

y          6771 ACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGGAG 6830
                |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
b          6781 ACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGGAG 6840

y          6831 ATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTG 6890
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          6841 ATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTG 6900

y          6891 GAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTACA 6950
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          6901 GAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTACA 6960

y          6951 AGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTC 7010
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          6961 AGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTC 7020

y          7011 TTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGATG 7070
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          7021 TTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGATG 7080

y          7071 GGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCT 7130
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          7081 GGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCT 7140

y          7131 GCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGGTG 7190
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          7141 GCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGGTG 7200

y          7191 AACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCATC 7250
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          7201 AACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCATC 7260

y          7251 AGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGG 7310
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          7261 AGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGG 7320

y          7311 CTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCT 7370
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         7321 CTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCT 7380

Qy         7371 CTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTCTT 7430
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         7381 CTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTCTT 7440

Qy         7431 TCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCTTC 7490
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         7441 TCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCTTC 7500

Qy         7491 TCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATTGC 7550
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         7501 TCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATTGC 7560

Qy         7551 CTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATT 7610
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         7561 CTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATT 7620

Qy         7611 TGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGA 7670
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         7621 TGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGA 7680

Qy         7671 TATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGTCT 7730
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         7681 TATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGTCT 7740

Qy         7731 GGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCACA 7790
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         7741 GGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCACA 7800

Qy         7791 GTA 7793
                |||
Db         7801 GTA 7803


RESULT 10
US-08-551-356-5
; Sequence 5, Application US/08551356
; Patent No. 5830700
;  GENERAL INFORMATION:
;    APPLICANT:  Irani, Meher
;    TITLE OF INVENTION:  HYBRID CROSS-LINKING PROTEINS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  4225 Roosevelt Way, N.E.
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/551,356
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/349,762
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/998,271
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Holly, Julie A
;      REGISTRATION NUMBER:  33-246
;      REFERENCE/DOCKET NUMBER:  92-26
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-547-8080 ext 322
;      TELEFAX:  206-548-2329
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  4027 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3..4013
US-08-551-356-5

  Query Match             28.4%;  Score 2211.8;  DB 2;  Length 4027;
  Best Local Similarity   89.9%;  Pred. No. 0;
  Matches 2499;  Conservative    0;  Mismatches    7;  Indels  273;  Gaps    1;

Qy       3199 CTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCTCAACAGACAACCAAACT 3258
              | | |||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CATGGCAGTGAGTCATGGGAGGGAGAGCAAGCCTCTGACTGCTCAACAGACAACCAAACT 61

Qy       3259 GGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCTACTGTCCTGGTGAGATG 3318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 GGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCTACTGTCCTGGTGAGATG 121

Qy       3319 GACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGTGGGCCTTACCCGAAGAGG 3378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGTGGGCCTTACCCGAAGAGG 181

Qy       3379 ACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTACCCACTGAGGAATCTGCA 3438
               |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        182 CCAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTACCCCCTGAGGAATCTGCA 241

Qy       3439 GCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGCAACCAAGAGAGCCCCAA 3498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGCAACCAAGAGAGCCCCAA 301

Qy       3499 AGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATTCCACCTTACAACACCGA 3558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 AGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATTCCACCTTACAACACCGA 361

Qy       3559 GGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCCAAGAATTGGTTTTAAGCT 3618
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        362 GGTGACTGAGACCACCATCGTGATCACATGGACGCCTGCTCCAAGAATTGGTTTTAAGCT 421

Qy       3619 GGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTGACTTCAGACTCAGGAAG 3678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTGACTTCAGACTCAGGAAG 481

Qy       3679 CATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTACACCATCCAAGTCCTGAG 3738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 CATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTACACCATCCAAGTCCTGAG 541

Qy       3739 AGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTGACACCATTGTCTCCACC 3798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 AGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTGACACCATTGTCTCCACC 601

Qy       3799 AACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTCACAGTCTCCTGGGAGAG 3858
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 AACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTCACAGTCTCCTGGGAGAG 661

Qy       3859 GAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACCCCTACAAACGGCCAGCA 3918
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Db        662 GAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACCCCTACAAACGGCCAGCA 721

Qy       3919 GGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCCTGCACTTTTGATAACCT 3978
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCCTGCACTTTTGATAACCT 781

Qy       3979 GAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAGGATGACAAGGAAAGTGT 4038
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAGGATGACAAGGAAAGTGT 841

Qy       4039 CCCTATCTCTGATACCATCATCCCA----------------------------------- 4063
              |||||||||||||||||||||||||
Db        842 CCCTATCTCTGATACCATCATCCCAGAGGTGCCCCAACTCACTGACCTAAGCTTTGTTGA 901

Qy       4064 ------------------------------------------------------------ 4063

Db        902 TATAACCGATTCAAGCATCGGCCTGAGGTGGACCCCGCTAAACTCTTCCACCATTATTGG 961

Qy       4064 ------------------------------------------------------------ 4063

Db        962 GTACCGCATCACAGTAGTTGCGGCAGGAGAAGGTATCCCTATTTTTGAAGATTTTGTGTA 1021

Qy       4064 ------------------------------------------------------------ 4063

Db       1022 CTCCTCAGTAGGATACTACACAGTCACAGGGCTGGAGCCGGGCATTGACTATGATATCAG 1081

Qy       4064 ----------------------------------------------------------GC 4065
                                                                        ||
Db       1082 CGTTATCACTCTCATTAATGGCGGCGAGAGTGCCCCTACTACACTGACACAACAAACGGC 1141

Qy       4066 TGTTCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCAC 4125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 TGTTCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCAC 1201

Qy       4126 CTGGGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAA 4185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 CTGGGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAA 1261

Qy       4186 AAATGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAAC 4245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 AAATGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAAC 1321

Qy       4246 AAATCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGA 4305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 AAATCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGA 1381

Qy       4306 GAGCACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTT 4365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 GAGCACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTT 1441

Qy       4366 TTCTGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCAC 4425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 TTCTGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCAC 1501

Qy       4426 TGGCTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGT 4485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1502 TGGCTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGT 1561

Qy       4486 GCCCCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGT 4545
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1562 GCCCCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGT 1621

Qy       4546 CAGCATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAAC 4605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1622 CAGCATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAAC 1681

Qy       4606 AGTTTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGAT 4665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1682 AGTTTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGAT 1741

Qy       4666 CAGCTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGG 4725
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1742 CAGCTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGG 1801

Qy       4726 AGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAG 4785
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1802 AGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAG 1861

Qy       4786 CGGCCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGA 4845
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1862 CGGCCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGA 1921

Qy       4846 CAGCCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATC 4905
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1922 CAGCCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATC 1981

Qy       4906 CCAGATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAG 4965
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1982 CCAGATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAG 2041

Qy       4966 TTCCCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAA 5025
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2042 TTCCCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAA 2101

Qy       5026 AACTAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGT 5085
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2102 AACTAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGT 2161

Qy       5086 GGAGTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCA 5145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2162 GGAGTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCA 2221

Qy       5146 GACTGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGA 5205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2222 GACTGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGA 2281

Qy       5206 TTCCATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTA 5265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2282 TTCCATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTA 2341

Qy       5266 CTCGAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACAC 5325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2342 CTCGAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACAC 2401

Qy       5326 TGCAGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCA 5385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2402 TGCAGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCA 2461

Qy       5386 CGATGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAAC 5445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2462 CGATGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAAC 2521

Qy       5446 TGACCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAA 5505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2522 TGACCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAA 2581

Qy       5506 TGTTCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAA 5565
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2582 TGTTCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAA 2641

Qy       5566 AGAAATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCAC 5625
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2642 AGAAATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCAC 2701

Qy       5626 CAAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGG 5685
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2702 CAAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGG 2761

Qy       5686 AGTTGTCACCACTCTGGAG 5704
               ||||||||||||||||||
Db       2762 TGTTGTCACCACTCTGGAG 2780

RESULT 11
PCT-US93-12687-5
; Sequence 5, Application PC/TUS9312687
;  GENERAL INFORMATION:
;    APPLICANT:  Irani, Meher H.
;    TITLE OF INVENTION:  HYBRID CROSS-LINKING PROTEINS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  4225 Roosevelt Way, N.E.
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/12687
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/998,271
;      FILING DATE:  31-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parker, Gary E
;      REGISTRATION NUMBER:  31-648
;      REFERENCE/DOCKET NUMBER:  92-26PC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-547-8080 ext 322
;      TELEFAX:  206-548-2329
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4027 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3..4013
PCT-US93-12687-5

  Query Match             28.4%;  Score 2211.8;  DB 5;  Length 4027;
  Best Local Similarity   89.9%;  Pred. No. 0;
  Matches 2499;  Conservative    0;  Mismatches    7;  Indels  273;  Gaps    1;

Qy       3199 CTTTGCAGTGAGCCATGGAGGGAGAGCAAGCCTCTGACTGCTCAACAGACAACCAAACT 3258
              | | |||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CATGGCAGTGAGTCATGGAGGGAGAGCAAGCCTCTGACTGCTCAACAGACAACCAAACT 61

Qy       3259 GGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCTACTGTCCTGGTGAGATG 3318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 GGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCTACTGTCCTGGTGAGATG 121

Qy       3319 GACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGTGGGCCTTACCCGAAGAGG 3378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGTGGGCCTTACCCGAAGAGG 181

Qy       3379 ACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTACCCACTGAGGAATCTGCA 3438
               |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        182 CCAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTACCCCCTGAGGAATCTGCA 241

Qy       3439 GCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGCAACCAAGAGAGCCCCAA 3498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGCAACCAAGAGAGCCCCAA 301

Qy       3499 AGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATTCCACCTTACAACACCGA 3558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 AGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATTCCACCTTACAACACCGA 361

Qy       3559 GGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCCAAGAATTGGTTTTAAGCT 3618
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        362 GGTGACTGAGACCACCATCGTGATCACATGGACGCCTGCTCCAAGAATTGGTTTTAAGCT 421

Qy       3619 GGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTGACTTCAGACTCAGGAAG 3678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTGACTTCAGACTCAGGAAG 481

Qy       3679 CATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTACACCATCCAAGTCCTGAG 3738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 CATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTACACCATCCAAGTCCTGAG 541

Qy       3739 AGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTGACACCATTGTCTCCACC 3798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 AGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTGACACCATTGTCTCCACC 601

Qy       3799 AACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTCACAGTCTCCTGGGAGAG 3858
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       602 AACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTCACAGTCTCCTGGGAGAG 661

Qy      3859 GAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACCCCTACAAACGGCCAGCA 3918
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       662 GAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACCCCTACAAACGGCCAGCA 721

Qy      3919 GGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCCTGCACTTTTGATAACCT 3978
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       722 GGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCCTGCACTTTTGATAACCT 781

Qy      3979 GAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAGGATGACAAGGAAAGTGT 4038
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       782 GAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAGGATGACAAGGAAAGTGT 841

Qy      4039 CCCTATCTCTGATACCATCATCCCA----------------------------------- 4063
             |||||||||||||||||||||||||
Db       842 CCCTATCTCTGATACCATCATCCCAGAGGTGCCCCAACTCACTGACCTAAGCTTTGTTGA 901

Qy      4064 ------------------------------------------------------------ 4063

Db       902 TATAACCGATTCAAGCATCGGCCTGAGGTGGACCCCGCTAAACTCTTCCACCATTATTGG 961

Qy      4064 ------------------------------------------------------------ 4063

Db       962 GTACCGCATCACAGTAGTTGCGGCAGGAGAAGGTATCCCTATTTTTGAAGATTTTGTGTA 1021

Qy      4064 ------------------------------------------------------------ 4063

Db      1022 CTCCTCAGTAGGATACTACACAGTCACAGGGCTGGAGCCGGGCATTGACTATGATATCAG 1081

Qy      4064 ----------------------------------------------------------GC 4065
                                                                       ||
Db      1082 CGTTATCACTCTCATTAATGGCGGCGAGAGTGCCCCTACTACACTGACACAACAAACGGC 1141

Qy      4066 TGTTCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCAC 4125
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1142 TGTTCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCAC 1201

Qy      4126 CTGGGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAA 4185
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1202 CTGGGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAA 1261

Qy      4186 AAATGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAAC 4245
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1262 AAATGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAAC 1321

Qy      4246 AAATCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGA 4305
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1322 AAATCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGA 1381

Qy      4306 GAGCACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTT 4365
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1382 GAGCACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTT 1441

Qy      4366 TTCTGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCAC 4425
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1442 TTCTGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCAC 1501

Qy      4426 TGGCTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGT 4485
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Db      1502 TGGCTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGT 1561

Qy      4486 GCCCCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGT 4545
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1562 GCCCCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGT 1621

Qy      4546 CAGCATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAAC 4605
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1622 CAGCATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAAC 1681

Qy      4606 AGTTTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGAT 4665
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1682 AGTTTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGAT 1741
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Qy      4666 CAGCTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGG 4725
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Db      1742 CAGCTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGG 1801

Qy      4726 AGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAG 4785
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1802 AGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAG 1861

Qy      4786 CGGCCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGA 4845
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1862 CGGCCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGA 1921

Qy      4846 CAGCCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATC 4905
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1922 CAGCCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATC 1981

Qy      4906 CCAGATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAG 4965
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1982 CCAGATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAG 2041

Qy      4966 TTCCCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAA 5025
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Db      2042 TTCCCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAA 2101

Qy      5026 AACTAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGT 5085
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Db      2102 AACTAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGT 2161

Qy      5086 GGAGTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCA 5145
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2162 GGAGTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCA 2221

Qy      5146 GACTGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGA 5205
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Db      2222 GACTGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGA 2281

Qy      5206 TTCCATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTA 5265
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Db      2282 TTCCATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTA 2341

Qy      5266 CTCGAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACAC 5325
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2342 CTCGAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACAC 2401

Qy      5326 TGCAGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCA 5385
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2402 TGCAGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCA 2461

Qy      5386 CGATGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAAC 5445
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2462 CGATGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAAC 2521

Qy      5446 TGACCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAA 5505
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2522 TGACCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAA 2581

Qy      5506 TGTTCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAA 5565
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2582 TGTTCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAA 2641

Qy      5566 AGAAATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCAC 5625
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Db      2642 AGAAATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCAC 2701

Qy      5626 CAAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGG 5685
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2702 CAAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGG 2761

Qy      5686 AGTTGTCACCACTCTGGAG 5704
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Db      2762 TGTTGTCACCACTCTGGAG 2780
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ESULT 12
S-09-366-009-20
 Sequence 20, Application US/09366009
 Patent No. 6426042
  GENERAL INFORMATION:
        APPLICANT: Asada, Kiyozo
                   Uemori, Takashi
                   Ueno, Takashi
                   Koyama, No. 6426042uto
                   Hashino, Kimikazu
                   Kato, Ikunoshin
        TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
                            CELLS WITH RETROVIRUS
        NUMBER OF SEQUENCES: 39
        CORRESPONDENCE ADDRESS:
              ADDRESSEE: WEISER & ASSOCIATES
              STREET: 230 South Fifteenth Street, Suite 500
              CITY: Philadelphia
              STATE: PA
              COUNTRY: USA
              ZIP: 19102
        COMPUTER READABLE FORM:
              MEDIUM TYPE: Floppy disk
              COMPUTER: IBM PC compatible
              OPERATING SYSTEM: PC-DOS/MS-DOS
              SOFTWARE: PatentIn Release #1.0, Version #1.30
        CURRENT APPLICATION DATA:
              APPLICATION NUMBER: US/09/366,009
              FILING DATE: 02-Aug-1999
              CLASSIFICATION: <Unknown>
        PRIOR APPLICATION DATA:
              APPLICATION NUMBER: 08/809,156
              FILING DATE: <Unknown>
              APPLICATION NUMBER: JP 294382/1995
              FILING DATE: 13-NOV-1995
              APPLICATION NUMBER: JP 051847/1996
              FILING DATE: 08-MAR-1996
        ATTORNEY/AGENT INFORMATION:
              NAME: Weiser, Gerard J.
              REGISTRATION NUMBER: 19,763
              REFERENCE/DOCKET NUMBER: 977.6507P
        TELECOMMUNICATION INFORMATION:
              TELEPHONE: 215-875-8383
              TELEFAX: 215-875-8394
  INFORMATION FOR SEQ ID NO: 20:
        SEQUENCE CHARACTERISTICS:
              LENGTH: 2481 base pairs
              TYPE: nucleic acid
              STRANDEDNESS: double
              TOPOLOGY: linear
        MOLECULE TYPE: DNA
        SEQUENCE DESCRIPTION: SEQ ID NO: 20:
S-09-366-009-20

 Query Match             18.0%;  Score 1400;  DB 4;  Length 2481;
 Best Local Similarity   76.7%;  Pred. No. 0;
 Matches 1895;  Conservative    0;  Mismatches  275;  Indels  300;  Gaps    3;

y         4071 CTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGG 4130
               ||   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
b            8 CTAGCCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGG 67

y         4131 CTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATG 4190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           68 CTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATG 127

y         4191 AGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATC 4250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          128 AGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATC 187

y         4251 TCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCA 4310
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         188 TCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCA 247

Qy        4311 CACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTG 4370
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         248 CACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTG 307

Qy        4371 ATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCT 4430
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Db         308 ATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCT 367

Qy        4431 ACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCC 4490
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Db         368 ACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCC 427

Qy        4491 ACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCA 4550
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Db         428 ACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCA 487

Qy        4551 TCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTT 4610
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         488 TCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTT 547

Qy        4611 CTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCT 4670
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         548 CTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCT 607

Qy        4671 GGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAA 4730
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         608 GGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAA 667

Qy        4731 ATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCC 4790
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         668 ATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCC 727

Qy        4791 TTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCC 4850
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         728 TTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCC 787

Qy        4851 CCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCC---- 4906
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         788 CCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCACTA 847

Qy        4907 --------------------CAGATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTG 4946
                                    |  || |  | ||  | ||      ||  ||| | || |
Db         848 GCGCTATTCCTGCACCAACTGACCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCG 907

Qy        4947 TCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAA 5006
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Db         908 CCCAGTGGACACCACCCAATGTTCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGG 967

Qy        5007 ATGGACCAGGACCAACAAAAACTAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTG 5066
               |     | |||||||  |||   |  |     | ||| ||     ||    ||  | |
Db         968 AGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTAT 1027

Qy        5067 AAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAGTGTCTATGCTC--------------- 5111
                |||  |   |    |     | ||||  || |||||||||||||
Db        1028 CAGGACTTATGGTGGCCACCAAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGA 1087

Qy        5112 ------------------------------------------------------------ 5111

Db        1088 CAAGCAGACCAGCTCAGGGTGTTGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGG 1147

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Qy        5112 ------------------------------------------------------------ 5111

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Qy        5112 ------------------------------------------------------------ 5111

Db        1268 CCATCAAGCCAGATGTCAGAAGCTACACCATCACAGGTTTACAACCAGGCACTGACTACA 1327
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Qy    5112 ------------------AGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAG 5153
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Db    1328 AGATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCT 1387

Qy    5154 TAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCA 5213
             ||   |||||||   ||       |||   |||   |          | ||||| |
Db    1388 CCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGC 1447

Qy    5214 AAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCC 5273
              |  | ||| |    ||||  |      || || | ||||   | |  ||   ||  |
Db    1448 TGGTATCATGGCAGCCGCCACGTGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGC 1507

Qy    5274 CTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGC 5333
           ||| |  |     |   ||  |  |||||   ||      ||  |        ||
Db    1508 CTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTA 1567

Qy    5334 TGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATA 5393
           |    |||||   ||||||  | || || ||| |   |||  ||||| || |  || ||
Db    1568 TTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAATC 1627

Qy    5394 TGGAGAGCCAGCCCCTGATTGGAACCC---AGTCCACAGCTATTCCTGCACCAACTGACC 5450
            | ||||| |||||||||||||||      || | |  ||||||||||||||||||||||
Db    1628 AGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACTAGCGCTATTCCTGCACCAACTGACC 1687

Qy    5451 TGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTC 5510
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1688 TGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTC 1747

Qy    5511 AGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAA 5570
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1748 AGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAA 1807

Qy    5571 TCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAAT 5630
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1808 TCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAAT 1867

Qy    5631 ATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTG 5690
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    1868 ATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGTTG 1927

Qy    5691 TCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGA 5750
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1928 TCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGA 1987

Qy    5751 CCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGATG 5810
           ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    1988 CCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATG 2047

Qy    5811 CCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCT 5870
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2048 CCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCT 2107

Qy    5871 ACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATG 5930
           |||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||
Db    2108 ACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATG 2167

Qy    5931 ACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCA 5990
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2168 ACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCA 2227

Qy    5991 ACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTG 6050
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2228 ACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTG 2287

Qy    6051 CCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGG 6110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2288 CCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGG 2347

Qy    6111 TCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCG 6170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2348 TCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCG 2407

Qy    6171 AATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAA 6230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2408 AATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAA 2467

Qy    6231 GGAAAAAGAC 6240
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Db    2468 GGAAAAAGAC 2477


RESULT 13
US-08-809-156B-20
; Sequence 20, Application US/08809156B
; Patent No. 6472204
;  GENERAL INFORMATION:
;    APPLICANT:  Asada, Kiyozo
;    APPLICANT:  Uemori, Takashi
;    APPLICANT:  Ueno, Takashi
;    APPLICANT:  Koyama, No. 6472204uto
;    APPLICANT:  Hashino, Kimikazu
;    APPLICANT:  Kato, Ikunoshin
;    TITLE OF INVENTION:  METHOD FOR GENE TRANSFER INTO TARGET
;    TITLE OF INVENTION:  CELLS WITH RETROVIRUS
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WEISER & ASSOCIATES
;      STREET:  230 South Fifteenth Street, Suite 500
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/809,156B
;      FILING DATE:  07-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP96/03254
;      FILING DATE:  07-NOV-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 294382/1995
;      FILING DATE:  13-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 051847/1996
;      FILING DATE:  08-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weiser, Gerard J.
;      REGISTRATION NUMBER:  19,763
;      REFERENCE/DOCKET NUMBER:  977.6507P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-875-8383
;      TELEFAX:  215-875-8394
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2481 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-809-156B-20

  Query Match             18.0%;  Score 1400;  DB 4;  Length 2481;
  Best Local Similarity   76.7%;  Pred. No. 0;
  Matches 1895;  Conservative    0;  Mismatches  275;  Indels  300;  Gaps    3;

Qy    4071 CTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGG 4130
           ||   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8 CTAGCCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGG 67

Qy    4131 CTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATG 4190
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     68 CTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATG 127

Qy   4191 AGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATC 4250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    128 AGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATC 187

Qy   4251 TCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCA 4310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    188 TCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCA 247

Qy   4311 CACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTG 4370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    248 CACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTG 307

Qy   4371 ATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCT 4430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    308 ATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCT 367

Qy   4431 ACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCC 4490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    368 ACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCC 427

Qy   4491 ACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCA 4550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    428 ACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCA 487

Qy   4551 TCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTT 4610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    488 TCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTT 547

Qy   4611 CTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCT 4670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    548 CTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCT 607

Qy   4671 GGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAA 4730
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    608 GGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAA 667

Qy   4731 ATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCC 4790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    668 ATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCC 727

Qy   4791 TTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCC 4850
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    728 TTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCC 787

Qy   4851 CCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCC---- 4906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    788 CCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCACTA 847

Qy   4907 --------------------CAGATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTG 4946
                               |  || |  | ||  | ||      ||  ||| | || |
Db    848 GCGCTATTCCTGCACCAACTGACCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCG 907

Qy   4947 TCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAA 5006
           | |||||   ||  | | |   |   | ||||| ||  ||||       || |||||
Db    908 CCCAGTGGACACCACCCAATGTTCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGG 967

Qy   5007 ATGGACCAGGACCAACAAAAACTAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTG 5066
          |     | |||||||  |||   |  |     | ||| ||     ||    ||  | |
Db    968 AGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTAT 1027

Qy   5067 AAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAGTGTCTATGCTC--------------- 5111
           |||  |   |    |     | ||||  || ||||||||||||||
Db   1028 CAGGACTTATGGTGGCCACCAAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGA 1087

Qy   5112 ------------------------------------------------------------ 5111

Db   1088 CAAGCAGACCAGCTCAGGGTGTTGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGG 1147

Qy   5112 ------------------------------------------------------------ 5111
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Db   1148 CTCGTGTGACAGATGCTACTGAGACCACCATCACCATTAGCTGGAGAACCAAGACTGAGA 1207

Qy   5112 ------------------------------------------------------------ 5111

Db   1208 CGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAA 1267

Qy   5112 ------------------------------------------------------------ 5111

Db   1268 CCATCAAGCCAGATGTCAGAAGCTACACCATCACAGGTTTACAACCAGGCACTGACTACA 1327

Qy   5112 ------------------AGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAG 5153
                             ||||   |  |    |||    ||| ||||        ||
Db   1328 AGATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCT 1387

Qy   5154 TAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCA 5213
            ||   |||||||   ||       |||   |||   |          | ||||| |
Db   1388 CCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGC 1447

Qy   5214 AAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCC 5273
             |  | ||| |    ||||  |      || || | ||||   | |  ||   ||  |
Db   1448 TGGTATCATGGCAGCCGCCACGTGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGC 1507

Qy   5274 CTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGC 5333
          ||| |  |     |   ||  |  |||||   ||      ||  |        ||
Db   1508 CTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTA 1567

Qy   5334 TGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATA 5393
          |    |||||   ||||||  | || || ||| |   |||  ||||| || |  || ||
Db   1568 TTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAATC 1627

Qy   5394 TGGAGAGCCAGCCCCTGATTGGAACCC---AGTCCACAGCTATTCCTGCACCAACTGACC 5450
           | ||||| ||||||||||||||      || | |  ||||||||||||||||||||||
Db   1628 AGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACTAGCGCTATTCCTGCACCAACTGACC 1687

Qy   5451 TGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTC 5510
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1688 TGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTC 1747

Qy   5511 AGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAA 5570
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1748 AGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAA 1807

Qy   5571 TCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAAT 5630
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1808 TCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAAT 1867

Qy   5631 ATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTG 5690
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   1868 ATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGTTG 1927

Qy   5691 TCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGA 5750
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1928 TCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGA 1987

Qy   5751 CCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGATG 5810
          ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   1988 CCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATG 2047

Qy   5811 CCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCT 5870
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2048 CCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCT 2107

Qy   5871 ACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATG 5930
          |||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||
Db   2108 ACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATG 2167

Qy   5931 ACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCA 5990
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2168 ACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCA 2227

Qy   5991 ACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTG 6050
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2228 ACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTG 2287
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Qy       6051 CCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGG 6110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2288 CCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGG 2347

Qy       6111 TCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCG 6170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2348 TCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCG 2407

Qy       6171 AATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAA 6230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2408 AATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAA 2467

Qy       6231 GGAAAAAGAC 6240
              ||||||||||
Db       2468 GGAAAAAGAC 2477

RESULT 14
US-09-366-009-33
; Sequence 33, Application US/09366009
; Patent No. 6426042
;  GENERAL INFORMATION:
;       APPLICANT: Asada, Kiyozo
;                  Uemori, Takashi
;                  Ueno, Takashi
;                  Koyama, No. 6426042uto
;                  Hashino, Kimikazu
;                  Kato, Ikunoshin
;       TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
;                           CELLS WITH RETROVIRUS
;       NUMBER OF SEQUENCES: 39
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: WEISER & ASSOCIATES
;            STREET: 230 South Fifteenth Street, Suite 500
;            CITY: Philadelphia
;            STATE: PA
;            COUNTRY: USA
;            ZIP: 19102
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/366,009
;            FILING DATE: 02-Aug-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/809,156
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: JP 294382/1995
;            FILING DATE: 13-NOV-1995
;            APPLICATION NUMBER: JP 051847/1996
;            FILING DATE: 08-MAR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Weiser, Gerard J.
;            REGISTRATION NUMBER: 19,763
;            REFERENCE/DOCKET NUMBER: 977.6507P
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 215-875-8383
;            TELEFAX: 215-875-8394
;  INFORMATION FOR SEQ ID NO: 33:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1722 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-366-009-33

  Query Match             11.8%;  Score 921.2;  DB 4;  Length 1722;
  Best Local Similarity   79.5%;  Pred. No. 2.1e-253;
  Matches 1130;  Conservative    0;  Mismatches  283;  Indels    9;  Gaps    3;

Qy       4900 ACCATCCCAGATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCC 4959
              ||||     |   |  ||||| |||| |   || | || ||| |   | |  |||    |
Db        300 ACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACCATTAGCTGGAGAAC 359

Qy       4960 TTCAAGTTCCCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACC 5019
                  | |    |  | ||||| | |  |||     ||  |||    ||||| |     ||
Db        360 CAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCCAATGGCCAGACTCC 419

Qy       5020 AACAAAAACTAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCC 5079
              ||   |    | |||       ||||||   | |      || ||   ||| || || ||
Db        420 AATCCA---GAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACAGGTTTACAACC 476

Qy       5080 CACAGTGGAGTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCT 5139
                     || ||   | |     | ||  |   ||||   |  |    |||    ||| |
Db        477 AGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTCCCCTGT 536

Qy       5140 GGTTCAGACTGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGA 5199
              |||       ||    ||   |||||||   ||       |||   |||   |
Db        537 GGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCACCAC 596

Qy       5200 TGTCGATTCCATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGT 5259
                 | ||||| |     |  | ||| |    ||||  |      || || | ||||   |
Db        597 ACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACCGGCTACATCAT 656

Qy       5260 GACCTACTCGAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGA 5319
               |  ||   ||  |||| |  |     |   ||  |  |||||   ||      ||  |
Db        657 CAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGGTGT 716

Qy       5320 AGACACTGCAGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGC 5379
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Db        717 CACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGC 776

Qy       5380 CTTGCACGATGATATGGAGAGCCAGCCCCTGATTGGAACCC---AGTCCACAGCTATTCC 5436
              | || |  || ||  | ||||| |||||||||||||||      || | |  ||||||||
Db        777 CCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACTAGCGCTATTCC 836

Qy       5437 TGCACCAACTGACCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGAC 5496
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Db        837 TGCACCAACTGACCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGAC 896

Qy       5497 ACCACCCAATGTTCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGG 5556
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Qy       5557 ACCAATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTAT 5616
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Db        957 ACCAATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTAT 1016

Qy       5617 GGTGGCCACCAAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACC 5676
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Qy       5677 AGCTCAGGGAGTTGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGAC 5736
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       5737 AGATGCTACTGAGACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGG 5796
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1137 AGATGCTACTGAGACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGG 1196

Qy       5797 CCTCCAAGTTGATGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCC 5856
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       5857 AGATGTCAGAAGCTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCT 5916
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Db       1257 AGATGTCAGAAGCTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCT 1316

Qy       5917 GTACACCTTGAATGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCAT 5976
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1317 GTACACCTTGAATGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCAT 1376

y       5977 TGATGCACCATCCAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATG 6036
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y       6037 GCAGCCGCCACGTGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCC 6096
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y       6097 TCCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCT 6156
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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y       6157 GGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGA 6216
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1557 GGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGA 1616

y       6217 GCCCCTGATTGGAAGGAAAAAGAC---AGACGAGCTTCCCCAACTGGTAACCCTTCCACA 6273
             ||||||||||||||||||||||||     |||||||||||||||||||||||||||||||
b       1617 GCCCCTGATTGGAAGGAAAAAGACTAGCGACGAGCTTCCCCAACTGGTAACCCTTCCACA 1676

y       6274 CCCCAATCTTCATGGACCAGAGATCTTGGATGTTCCTTCCAC 6315
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b       1677 CCCCAATCTTCATGGACCAGAGATCTTGGATGTTCCTTCCAC 1718

ESULT 15
S-08-809-156B-33
 Sequence 33, Application US/08809156B
 Patent No. 6472204
  GENERAL INFORMATION:
    APPLICANT:  Asada, Kiyozo
    APPLICANT:  Uemori, Takashi
    APPLICANT:  Ueno, Takashi
    APPLICANT:  Koyama, No. 6472204uto
    APPLICANT:  Hashino, Kimikazu
    APPLICANT:  Kato, Ikunoshin
    TITLE OF INVENTION:  METHOD FOR GENE TRANSFER INTO TARGET
    TITLE OF INVENTION:  CELLS WITH RETROVIRUS
    NUMBER OF SEQUENCES:  39
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  WEISER & ASSOCIATES
      STREET:  230 South Fifteenth Street, Suite 500
      CITY:  Philadelphia
      STATE:  PA
      COUNTRY:  USA
      ZIP:  19102
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/809,156B
;     FILING DATE:  07-MAR-1997
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/JP96/03254
;     FILING DATE:  07-NOV-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  JP 294382/1995
;     FILING DATE:  13-NOV-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  JP 051847/1996
;     FILING DATE:  08-MAR-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Weiser, Gerard J.
;     REGISTRATION NUMBER:  19,763
;     REFERENCE/DOCKET NUMBER:  977.6507P
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  215-875-8383
;     TELEFAX:  215-875-8394
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1722 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-809-156B-33

  Query Match             11.8%;  Score 921.2;  DB 4;  Length 1722;
  Best Local Similarity   79.5%;  Pred. No. 2.1e-253;
  Matches 1130;  Conservative    0;  Mismatches  283;  Indels    9;  Gaps    3;

Qy       4900 ACCATCCCAGATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCC 4959
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Db        300 ACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACCATTAGCTGGAGAAC 359

Qy       4960 TTCAAGTTCCCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACC 5019
                  | |    |  | ||||| | |  |||     ||  |||    ||||| |     ||
Db        360 CAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCCAATGGCCAGACTCC 419

Qy       5020 AACAAAAACTAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCC 5079
              ||   |    | |||       ||||||   | |      || ||   ||| || || ||
Db        420 AATCCA---GAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACAGGTTTACAACC 476

Qy       5080 CACAGTGGAGTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCT 5139
                     || ||   | |     | ||  |   ||||   |  |    |||    ||| |
Db        477 AGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTCCCCTGT 536

Qy       5140 GGTTCAGACTGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGA 5199
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Db        597 ACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACCGGCTACATCAT 656

Qy       5260 GACCTACTCGAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGA 5319
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Db        957 ACCAATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTAT 1016

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Qy       5677 AGCTCAGGGAGTTGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGAC 5736
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```

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Qy       5797 CCTCCAAGTTGATGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCC 5856
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Qy       5917 GTACACCTTGAATGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCAT 5976
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Qy       5977 TGATGCACCATCCAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATG 6036
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Qy       6037 GCAGCCGCCACGTGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCC 6096
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Qy       6097 TCCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCT 6156
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Db       1617 GCCCCTGATTGGAAGGAAAAAGACTAGCGACGAGCTTCCCCAACTGGTAACCCTTCCACA 1676

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Search completed: March  7, 2004, 21:48:28
Job time : 595 secs
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                    GenCore version 5.1.6
           Copyright (c) 1993 - 2004  Compugen Ltd.

M nucleic - nucleic search, using sw model

un on:          March  7, 2004, 05:41:46 ; Search time 2538 Seconds
                                           (without alignments)
                                           13047.559 Million cell updates/sec

itle:           US-10-084-817-2
erfect score:   7795
equence:        1 cggctcgagccggctgtgct..........ttttaaatatccacagtact 7795

coring table:   IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

earched:        3373863 seqs, 2124099041 residues

otal number of hits satisfying chosen parameters:      6747726

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                1:  geneseqn1980s:*
                2:  geneseqn1990s:*
                3:  geneseqn2000s:*
                4:  geneseqn2001as:*
                5:  geneseqn2001bs:*
                6:  geneseqn2002s:*
                7:  geneseqn2003as:*
                8:  geneseqn2003bs:*
                9:  geneseqn2003cs:*
                10:  geneseqn2004s:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                   SUMMARIES
                     %
esult               Query
  No.    Score     Match Length DB  ID                         Description
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     1  7780.6    99.8    8044  6  AAS94866                  Aas94866 Human DNA
     2  7774.8    99.7    8137  4  AAI57805                  Aai57805 Human pol
     3  7671.8    98.4    8230  4  AAI57804                  Aai57804 Human pol
     4  7614.8    97.7    8062  4  AAI57802                  Aai57802 Human pol
     5    7423    95.2    7679  9  ADB31322                  Adb31322 Testoster
     6    7423    95.2    7680  3  AAF21131                  Aaf21131 Human low
     7    7423    95.2    7680  5  ABA82689                  Aba82689 Fibronect
     8    7423    95.2    7680  6  ABL67540                  Abl67540 Thyroid c
     9    7423    95.2    7680  6  ABT11082                  Abt11082 Human bre
    10    7423    95.2    7680  7  ABZ96825                  Abz96825 Human nuc
    11    7423    95.2    7680  7  ACF03878                  Acf03878 Human fib
    12    7423    95.2    7680  7  ABX10391                  Abx10391 DNA encod
    13    7423    95.2    7680  7  ACC46009                  Acc46009 Human fib
    14    7423    95.2    7680  7  ACF12859                  Acf12859 Human cer
    15    7423    95.2    7680  7  ACA64817                  Aca64817 Human fib
    16    7423    95.2    7680  7  ACA64819                  Aca64819 Human fib
    17    7423    95.2    7680  8  ADB70377                  Adb70377 Fibronect
    18    7423    95.2    7680  9  ADB98703                  Adb98703 Human fib
    19    7423    95.2    7680  9  ADD18771                  Add18771 Human dis
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    22    7423    95.2   14740  3  AAF21132                  Aaf21132 Human low
    23    7423    95.2   14740  7  ABZ96826                  Abz96826 Human nuc
    24  7419.8    95.2    7680  2  AAT17551                  Aat17551 Human fib
    25  7418.2    95.2    7705  1  AAN70596                  Aan70596 Sequence
    26    7415    95.1    7705  2  AAQ15214                  Aaq15214 Human fib
c   27  7410.4    95.1    8066  4  AAI59591                  Aai59591 Human pol
c   28  7410.4    95.1    8066  4  AAI59589                  Aai59589 Human pol
c   29  7410.4    95.1    8066  4  AAI59588                  Aai59588 Human pol
c   30  7410.4    95.1    8066  4  AAI59590                  Aai59590 Human pol
    31  7341.6    94.2    7705  2  AAQ05502                  Aaq05502 Sequence
    32    7237    92.8    8039  3  AAC89889                  Aac89889 Human FN
    33  7224.8    92.7    7867  4  AAI57803                  Aai57803 Human pol
    34    7223    92.7    7803  2  AAQ70009                  Aaq70009 Fibrinoge
    35    7218    92.6    7550  7  ACC00412                  Acc00412 Human cel
    36    6964    89.3    6988  8  ACD06169                  Acd06169 Human cDN
    37  6844.4    87.8    8216  5  AAS86466                  Aas86466 DNA encod
    38  5869.4    75.3    7361  8  ACD06170                  Acd06170 Human cDN
    39  5320.6    68.3    8329  6  ABK63824                  Abk63824 Rat seque
    40  5320.6    68.3    8329  9  ADB58331                  Adb58331 Toxicity-
    41  5320.6    68.3    8329  9  ADB52891                  Adb52891 Primary r
    42  5185.2    66.5    6816  7  ABX74443                  Abx74443 Human cDN
    43  3466.2    44.5    4860  3  AAA35009                  Aaa35009 Human ade
    44  2963.8    38.0    3522  5  AAS86462                  Aas86462 DNA encod
    45  2211.8    28.4    4027  2  AAQ70007                  Aaq70007 Tissue-bi


                                   ALIGNMENTS


RESULT 1
AAS94866
ID   AAS94866 standard; DNA; 8044 BP.
XX
AC   AAS94866;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Human DNA sequence #121 expressed during foam cell differentiation.
XX
KW   Human; foam cell differentiation; atherosclerosis; cerebral stroke;
KW   cardiovascular disorder; coronary artery disease; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200177389-A2.
XX
PD   18-OCT-2001.
XX
PF   04-APR-2001; 2001WO-US011128.
XX
PR   05-APR-2000; 2000US-0195106P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Shiffman D,  Somogyi R,  Lawn R,  Seilhamer JJ,  Porter GJ,  Mikita T;
PI   Tai J;
XX
DR   WPI; 2002-010925/01.
XX
PT   Composition useful for diagnosis of conditions, disorders or diseases
PT   associated with atherosclerosis, comprises several polynucleotides that
PT   are differentially expressed in foam cell development.
XX
PS   Claim 1; Page 175-177; 315pp; English.
XX
CC   The present invention relates to the isolation of human polynucleotide
CC   sequences that are differentially expressed during foam cell
CC   differentiation. The polynucleotide sequences of the invention or a
CC   composition comprising these polynucleotides are useful as a high
CC   throughput method for detecting altered expression of one or more
CC   polynucleotides in a sample. The polynucleotides can be used in the
CC   diagnosis of disorders associated with foam cell development such as
CC   atherosclerosis, cerebral stroke, and cardiovascular disorders such as
CC   coronary artery disease. The polynucleotide sequences can also be used as
CC   PCR primers and probes. The polynucleotides of the invention are also
CC   useful in gene therapy. AAS94746-AAS95021 represent the human
CC   polynucleotide sequences of the invention which are differentially
CC   expressed during foam cell differentiation
XX
SQ   Sequence 8044 BP; 2143 A; 2107 C; 1977 G; 1817 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 7780.6;  DB 6;  Length 8044;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7786;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 CGGCTCGAGCCGGCTGTGCTGCACAGGGGGAGGAGAGGGAACCCCAGGCGCGAGCGGGAA 60
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Qy         61 GAGGGGACCTGCAGCCACAACTTCTCTGGTCCTCTGCATCCCTTCTGTCCCTCCACCCGT 120
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Qy        121 CCCCTTCCCCACCCTCTGGCCCCCACCTTCTTGGAGGCGACAACCCCCGGGAGGCATTAG 180
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Db        121 CCCCTTCCCCACCCTCTGGCCCCCACCTTCTTGGAGGCGACAACCCCCGGGAGGCATTAG 180

Qy        181 AAGGGATTTTTCCCGCAGGTTGCGAAGGGAAGCAAACTTGGTGGCAACTTGCCTCCCGGT 240
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Db        181 AAGGGATTTTTCCCGCAGGTTGCGAAGGGAAGCAAACTTGGTGGCAACTTGCCTCCCGGT 240

Qy        241 GCGGGCGTCTCTCCCCCACCGTCTCAACATGCTTAGGGGTCCGGGGCCCGGGCTGCTGCT 300
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Qy        301 GCTGGCCGTCCTGTGCCTGGGGACAGCGGTGCCCTCCACGGGAGCCTCGAAGAGCAAGAG 360
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Db        301 GCTGGCCGTCCTGTGCCTGGGGACAGCGGTGCCCTCCACGGGAGCCTCGAAGAGCAAGAG 360

Qy        361 GCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCGG 420
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Db        361 GCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCGG 420

Qy        421 TTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGG 480

Qy        481 CAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAACC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        481 CAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAGAGTAAACC 540

Qy        541 TGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACAC 600

Qy        601 TTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGG 660
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        601 TTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATTGGGGCTGGGCGAGG 660

Qy        661 GAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGG 720

Qy        721 TGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTGTGTGTGTCTTGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTGTGTGTGTCTTGG 780

Qy        781 TAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGC 840

Qy        841 TGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGT 900

Qy        901 AGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATG 960

Qy        961 CAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAA 1020

Qy       1021 TCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGA 1080

Qy       1081 GAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTGC 1140

Qy       1141 AGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCACTGTGTCACAGA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCACTGTGTCACAGA 1200

Qy       1201 CAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGGAAATAAGCAAAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGGAAATAAGCAAAT 1260

Qy       1261 GCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGTAACCCAGACTTA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGTAACCCAGACTTA 1320

Qy       1321 CGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAATGGCAGGACGTT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAATGGCAGGACGTT 1380

Qy       1381 CTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAGCACAACTTCGAA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAGCACAACTTCGAA 1440

Qy       1441 TTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTTGGTTCAGACTCG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTTGGTTCAGACTCG 1500

Qy       1501 AGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAACAACCACAATTA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAACAACCACAATTA 1560

Qy       1561 CACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGGGACCACACAGAA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGGGACCACACAGAA 1620

Qy       1621 CTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGAGGAAATCTGCAC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGAGGAAATCTGCAC 1680

Qy       1681 AACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCAGCATGACATGGG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 AACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCAGCATGACATGGG 1740

Qy       1741 TCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGACATGCATTGCCTA 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGACATGCATTGCCTA 1800

Qy       1801 CTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATT 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATT 1860

Qy       1861 CCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGG 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGG 1920

Qy       1921 CAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCA 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCA 1980

Qy       1981 AATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGG 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 AATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGG 2040
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Qy   2041 CCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCC 2100

Qy   2101 TGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAA 2160

Qy   2161 TGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGT 2220

Qy   2221 AGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 AGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCT 2280

Qy   2281 GAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGA 2340

Qy   2341 AGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGACCAGCAACACCGT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGACCAGCAACACCGT 2400

Qy   2401 GACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAAT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAAT 2460

Qy   2461 CACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCG 2520

Qy   2521 GGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCAC 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 GGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCAC 2580

Qy   2581 AGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 AGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTA 2640

Qy   2641 TCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 TCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCC 2700

Qy   2701 TGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 TGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTG 2760

Qy   2761 GAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 GAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGG 2820

Qy   2821 TAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCA 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCA 2880

Qy   2881 ACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 ACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACC 2940

Qy   2941 TGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAG 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 TGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAG 3000

Qy   3001 GGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGA 3060

Qy   3061 GAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 GAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGG 3120

Qy   3121 GCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGT 3180

Qy   3181 CACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGC 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 CACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGC 3240

Qy   3241 TCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTC 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTC 3300

Qy   3301 TACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGT 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 TACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGT 3360

Qy   3361 GGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTA 3420
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   3361 GGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTA 3420

Qy   3421 CCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGG 3480
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 CCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGG 3480

Qy   3481 CAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTAT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTAT 3540

Qy   3541 TCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCC 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCC 3600

Qy   3601 AAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 AAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGT 3660

Qy   3661 GACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTA 3720

Qy   3721 CACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGT 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 CACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGT 3780

Qy   3781 GACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCT 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCT 3840

Qy   3841 CACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAAC 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 CACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAAC 3900

Qy   3901 CCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTC 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 CCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTC 3960

Qy   3961 CTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAA 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAA 4020

Qy   4021 GGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCAC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 GGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCAC 4080

Qy   4081 TGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCC 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 TGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCC 4140

Qy   4141 ATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGT 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 ATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGT 4200

Qy   4201 TGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGG 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 TGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGG 4260

Qy   4261 TACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAG 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 TACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAG 4320

Qy   4321 AGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGC 4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 AGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGC 4380

Qy   4381 CAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCG 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 CAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCG 4440

Qy   4441 CCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAA 4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 CCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAA 4500

Qy   4501 TTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCT 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 TTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCT 4560

Qy   4561 TAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCC 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 TAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCC 4620

Qy   4621 GAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCC 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 GAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCC 4680

Qy   4681 TGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGT 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 TGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGT 4740

Qy   4741 CCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGG 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 CCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGG 4800

Qy   4801 AGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAG 4860
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Db   4801 AGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAG 4860

Qy   4861 CAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGAC 4920
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Db   4861 CAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGAC 4920

Qy   4921 CGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGG 4980
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Qy   4981 TTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGG 5040
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Db   4981 TTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGG 5040

Qy   5041 TCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAG 5100
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Db   5041 TCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAG 5100

Qy   5101 TGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAA 5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 TGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAA 5160

Qy   5161 CATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGC 5220
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Db   5161 CATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGC 5220

Qy   5221 TTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGA 5280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 TTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGA 5280

Qy   5281 TGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGG 5340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5281 TGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGG 5340

Qy   5341 CCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAG 5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 CCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAG 5400

Qy   5401 CCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCAC 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5401 CCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCAC 5460

Qy   5461 TCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGG 5520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 TCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGG 5520

Qy   5521 ATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGC 5580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5521 ATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGC 5580

Qy   5581 TCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAG 5640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 TCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAG 5640

Qy   5641 TGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTGTCACCACTCT 5700
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   5641 TGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGTTGTCACCACTCT 5700

Qy   5701 GGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCAC 5760
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Db   5701 GGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCAC 5760

Qy   5761 CATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGATGCCGTTCCAGC 5820
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   5761 CATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGC 5820

Qy   5821 CAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCAC 5880
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Db   5821 CAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCAC 5880

Qy   5881 TGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCG 5940
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Db   5881 AGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCG 5940

Qy   5941 GAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTT 6000
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Db   5941 GAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTT 6000

Qy   6001 CCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTAC 6060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6001 CCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTAC 6060

Qy   6061 CGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCC 6120
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Db   6061 CGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCC 6120

Qy   6121 CCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAAT 6180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6121 CCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAAT 6180

Qy   6181 TTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGAC 6240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6181 TTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGAC 6240

Qy   6241 AGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTT 6300
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Qy   6301 GGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGG 6360
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Db   6301 GGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGG 6360

Qy   6361 AAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGAT 6420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6361 AAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGAT 6420
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Qy       6421 CTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCA 6480
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Db       6421 CTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCA 6480

Qy       6481 TAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTC 6540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 TAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTC 6540

Qy       6541 ATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTGTTGGCACTGA 6600
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Qy       6601 TGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTCTGACAGGCCT 6660
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Qy       6661 CACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAA 6720
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Db       6661 CACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAA 6720

Qy       6721 GGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTAC 6780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6721 GGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTAC 6780

Qy       6781 GGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGGAGATGAGTGGGA 6840
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       6781 GGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGGAGATGAGTGGGA 6840

Qy       6841 ACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCA 6900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6841 ACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCA 6900

Qy       6901 TTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGA 6960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6901 TTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGA 6960

Qy       6961 GAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTCTTGGGAACGG 7020
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Db       6961 GAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTCTTGGGAACGG 7020

Qy       7021 AAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGATGGGAAGACATA 7080
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Qy       7081 CCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTT 7140
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Db       7081 CCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTT 7140

Qy       7141 TGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGGTGAACCCAGTCC 7200
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Qy       7201 CGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCATCAGAGAACAAA 7260
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Qy       7261 CACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGGCTGACAGAGA 7320
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Qy       7321 AGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCTCTCTGCCAAG 7380
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Db       7321 AGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCTCTCTGCCAAG 7380

Qy       7381 ATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTCTTTCTTTCTTAA 7440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7381 ATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTCTTTCTTTCTTAA 7440

Qy       7441 GCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCTTCTCCAAGCATC 7500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7441 GCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCTTCTCCAAGCATC 7500

Qy       7501 ACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATTGCCTGTTCTGCT 7560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7501 ACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATTGCCTGTTCTGCT 7560

Qy       7561 TCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATTTGGTTTGGGA 7620
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Db       7561 TCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATTTGGTTTGGGA 7620

Qy       7621 TCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGATATGACCAAA 7680
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Db       7621 TCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGATATGACCAAA 7680

Qy       7681 ATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGTCTGGCCCGCAAT 7740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7681 ATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGTCTGGCCCGCAAT 7740

Qy       7741 ACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCACAGTACT 7795
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7741 ACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCACAGTACT 7795


RESULT 2
AAI57805
ID   AAI57805 standard; cDNA; 8137 BP.
XX
AC   AAI57805;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 8.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US034263.
XX
PR   23-DEC-1999;   99US-00471275.
PR   21-JAN-2000; 2000US-00488725.
PR   25-APR-2000; 2000US-00552317.
PR   20-JUN-2000; 2000US-00598042.
PR   19-JUL-2000; 2000US-00620312.
PR   03-AUG-2000; 2000US-00653450.
PR   14-SEP-2000; 2000US-00662191.
PR   19-OCT-2000; 2000US-00693036.
PR   29-NOV-2000; 2000US-00727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J,  Zhao QA;
PI   Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   P-PSDB; AAM38649.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders such
PT   as central nervous system injuries.
XX
PS   Claim 1; SEQ ID NO 8; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC   encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders. Note: The sequence data for this patent did not form
CC   part of the printed specification
XX
SQ   Sequence 8137 BP; 2182 A; 2126 C; 1992 G; 1837 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 7774.8;  DB 4;  Length 8137;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7779;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         10 CCGGCTGTGCTGCACAGGGGGAGGAGAGGGAACCCCAGGCGCGAGCGGGAAGAGGGGACC 69
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Db        104 CCGGCTGTGCTGCACAGGGGGAGGAGAGGGAACCCCAGGCGCGAGCGGGAAGAGGGGACC 163

Qy         70 TGCAGCCACAACTTCTCTGGTCCTCTGCATCCCTTCTGTCCCTCCACCCGTCCCCTTCCC 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 TGCAGCCACAACTTCTCTGGTCCTCTGCATCCCTTCTGTCCCTCCACCCGTCCCCTTCCC 223

Qy        130 CACCCTCTGGCCCCCACCTTCTTGGAGGCGACAACCCCCGGGAGGCATTAGAAGGGATTT 189
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Db        224 CACCCTCTGGCCCCCACCTTCTTGGAGGCGACAACCCCCGGGAGGCATTAGAAGGGATTT 283

Qy        190 TTCCCGCAGGTTGCGAAGGGAAGCAAACTTGGTGGCAACTTGCCTCCCGGTGCGGGCGTC 249
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Qy        250 TCTCCCCCACCGTCTCAACATGCTTAGGGGTCCGGGGCCCGGGCTGCTGCTGCTGGCCGT 309
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Db        344 TCTCCCCCACCGTCTCAACATGCTTAGGGGTCCGGGGCCCGGGCTGCTGCTGCTGGCCGT 403

Qy        310 CCTGTGCCTGGGGACAGCGGTGCCCTCCACGGGAGCCTCGAAGAGCAAGAGGCAGGCTCA 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 CCTGTGCCTGGGGACAGCGGTGCCCTCCACGGGAGCCTCGAAGAGCAAGAGGCAGGCTCA 463

Qy        370 GCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCGGTTGTTATGA 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 GCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCGGTTGTTATGA 523

Qy        430 CAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGCAATGCGTT 489
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Db        524 CAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGCAATGCGTT 583

Qy        490 GGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAACCTGAAGCTGA 549
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Db        584 GGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAGAGTAAACCTGAAGCTGA 643

Qy        550 AGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACACTTATGAGCG 609
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Db        644 AGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACACTTATGAGCG 703

Qy        610 TCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGGAGAATAAG 669
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Db        704 TCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGGAGAATAAG 763

Qy        670 CTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGGTGACACCTG 729
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Db        764 CTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGGTGACACCTG 823

Qy        730 GAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTGTGTGTGTCTTGGTAATGGAAA 789
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Db        824 GAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTGTGTGTGTCTTGGTAATGGAAA 883

Qy        790 AGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTC 849
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Db        884 AGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTC 943
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Qy        850 CTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTAC 909
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Qy        910 TTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCA 969
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Db       1004 TTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCA 1063

Qy        970 GGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAA 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 GGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAA 1123

Qy       1030 CCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACAC 1089
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Db       1124 CCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACAC 1183

Qy       1090 CTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTGCAGCTGTTTA 1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1210 GGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGGAAATAAGCAAATGCTTTGCAC 1269
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Db       1304 GGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGGAAATAAGCAAATGCTTTGCAC 1363

Qy       1270 GTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGTAACCCAGACTTACGGTGGCAA 1329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1364 GTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGTAACCCAGACTTACGGTGGCAA 1423

Qy       1330 CTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAATGGCAGGACGTTCTACTCCTG 1389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1424 CTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAATGGCAGGACGTTCTACTCCTG 1483

Qy       1390 CACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAGCACAACTTCGAATTATGAGCA 1449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1484 CACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAGCACAACTTCGAATTATGAGCA 1543

Qy       1450 GGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTTGGTTCAGACTCGAGGAGGAAA 1509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1544 GGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTTGGTTCAGACTCGAGGAGGAAA 1603

Qy       1510 TTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAACAACCACAATTACACTGATTG 1569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1604 TTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAACAACCACAATTACACTGATTG 1663

Qy       1570 CACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGGGACCACACAGAACTATGATGC 1629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1664 CACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGGGACCACACAGAACTATGATGC 1723

Qy       1630 CGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGAGGAAATCTGCACAACCAATGA 1689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1724 CGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGAGGAAATCTGCACAACCAATGA 1783

Qy       1690 AGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCAGCATGACATGGGTCACATGAT 1749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1784 AGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCAGCATGACATGGGTCACATGAT 1843

Qy       1750 GAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGACATGCATTGCCTACTCGCAGCT 1809
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1844 GAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGACATGCATTGCCTACTCGCAACT 1903

Qy       1810 TCGAGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATTCCACAAGCG 1869
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1904 TCGAGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATTCCACAAGCG 1963

Qy       1870 TCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGCAGGTGGAA 1929
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1964 TCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGCAGGTGGAA 2023
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Qy      1930 GTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCAAATTGGAGA 1989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2024 GTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCAAATTGGAGA 2083

Qy      1990 TTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGCCGTGGCAT 2049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2084 TTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGCCGTGGCAT 2143

Qy      2050 TGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCCTGTCGAAGT 2109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2144 TGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCCTGTCGAAGT 2203

Qy      2110 ATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAATGCACCACA 2169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2204 ATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAATGCACCACA 2263

Qy      2170 GCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTAGGCCGTTG 2229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2264 GCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTAGGCCGTTG 2323

Qy      2230 GAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTGAAGCCTGG 2289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2324 GAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTGAAGCCTGG 2383

Qy      2290 TGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAAGTGACTCG 2349
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2384 TGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAAGTGACTCG 2443

Qy      2350 CTTTGACTTCACCACCACCAGCACCAGCACACCTGTGACCAGCAACACCGTGACAGGAGA 2409
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2444 CTTTGACTTCACCACCACCAGCACCAGCACACCTGTGACCAGCAACACCGTGACAGGAGA 2503

Qy      2410 GACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATCACAGCCAG 2469
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2504 GACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATCACAGCCAG 2563

Qy      2470 TAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGGGTGGAATA 2529
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2564 TAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGGGTGGAATA 2623

Qy      2530 TGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACAGCCACTTC 2589
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2624 TGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACAGCCACTTC 2683

Qy      2590 TGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTATCAGATATC 2649
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2684 TGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTATCAGATATC 2743

Qy      2650 TGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCCTGATGCCCC 2709
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2744 TGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCCTGATGCCCC 2803

Qy      2710 TCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGGAGCAGACC 2769
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2804 TCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGGAGCAGACC 2863

Qy      2770 CCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGTAGCAGCAC 2829
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2864 CCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGTAGCAGCAC 2923

Qy      2830 AGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAACCTGGTGT 2889
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2924 AGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAACCTGGTGT 2983

Qy      2890 TCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCTGTTGTCAT 2949
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2984 TCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCTGTTGTCAT 3043

Qy      2950 TCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGGGACCTGCA 3009
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3044 TCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGGGACCTGCA 3103

Qy      3010 GTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAGAGTGCAGT 3069
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3104 GTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAGAGTGCAGT 3163

Qy      3070 GACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGGCAGAGGCT 3129
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3164 GACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGGCAGAGGCT 3223

Qy      3130 GCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTCACCTATTA 3189
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3224 GCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTCACCTATTA 3283

Qy      3190 CTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCTCAACAGAC 3249
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3284 CTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCTCAACAGAC 3343

Qy      3250 AACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCTACTGTCCT 3309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3344 AACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCTACTGTCCT 3403

Qy      3310 GGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGTGGGCCTTAC 3369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3404 GGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGTGGGCCTTAC 3463

Qy      3370 CCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTACCCACTGAG 3429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3464 CCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTACCCACTGAG 3523

Qy      3430 GAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGCAACCAAGA 3489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3524 GAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGCAACCAAGA 3583

Qy      3490 GAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATTCCACCTTA 3549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3584 GAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATTCCACCTTA 3643

Qy      3550 CAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCCAAGAATTGG 3609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3644 CAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCCAAGAATTGG 3703

Qy      3610 TTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTGACTTCAGA 3669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3704 TTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTGACTTCAGA 3763

Qy      3670 CTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTACACCATCCA 3729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3764 CTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTACACCATCCA 3823

Qy      3730 AGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTGACACCATT 3789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3824 AGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTGACACCATT 3883

Qy      3790 GTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTCACAGTCTC 3849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3884 GTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTCACAGTCTC 3943

Qy      3850 CTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACCCCTACAAA 3909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3944 CTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACCCCTACAAA 4003

Qy      3910 CGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCCTGCACTTT 3969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4004 CGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCCTGCACTTT 4063

Qy      3970 TGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAGGATGACAA 4029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4064 TGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAGGATGACAA 4123

Qy      4030 GGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCACTGACCTGCG 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4124 GGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCACTGACCTGCG 4183

Qy      4090 ATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCCATCCATTGA 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4184 ATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCCATCCATTGA 4243

Qy   4150 TTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGTTGCAGAGTT 4209
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4244 TTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGTTGCAGAGTT 4303

Qy   4210 GTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGGTACAGAATA 4269
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4304 GTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGGTACAGAATA 4363

Qy   4270 TGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGAGGAAGACA 4329
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4364 TGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGAGGAAGACA 4423

Qy   4330 GAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGCCAACTCTTT 4389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4424 GAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGCCAACTCTTT 4483

Qy   4390 TACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGCCATCATCC 4449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4484 TACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGCCATCATCC 4543

Qy   4450 CGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAATTCCATCAC 4509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4544 CGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAATTCCATCAC 4603

Qy   4510 CCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCTTAATGGCAG 4569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4604 CCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCTTAATGGCAG 4663

Qy   4570 AGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCGAGGGACCT 4629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4664 AGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCGAGGGACCT 4723

Qy   4630 GGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCCTGCTGTCAC 4689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4724 GGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCCTGCTGTCAC 4783

Qy   4690 AGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGTCCAGGAGTT 4749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4784 AGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGTCCAGGAGTT 4843

Qy   4750 CACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGGAGTTGATTA 4809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4844 CACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGGAGTTGATTA 4903

Qy   4810 TACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGCAAGCCAAT 4869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4904 TACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGCAAGCCAAT 4963

Qy   4870 TTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTCA 4929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4964 TTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTCA 5023

Qy   4930 GGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGTTACAGAGT 4989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5024 GGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGTTACAGAGT 5083

Qy   4990 AACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGGTCCAGATCA 5049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5084 AACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGGTCCAGATCA 5143

Qy   5050 AACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAGTGTCTATGC 5109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5144 AACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAGTGTCTATGC 5203

Qy   5110 TCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAACATTGATCG 5169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5204 TCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAACATTGATCG 5263

Qy   5170 CCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGCTTGGGAAAG 5229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5264 CCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGCTTGGGAAAG 5323

Qy   5230 CCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGATGGAATCCA 5289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5324 CCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGATGGAATCCA 5383

Qy   5290 TGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGCCTCAGACC 5349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5384 TGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGCCTCAGACC 5443

Qy   5350 GGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAGCCAGCCCCT 5409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5444 GGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAGCCAGCCCCT 5503

Qy   5410 GATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCACTCAGGTCAC 5469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5504 GATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCACTCAGGTCAC 5563

Qy   5470 ACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGGATATCGAGT 5529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5564 ACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGGATATCGAGT 5623

Qy   5530 GCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAG 5589
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5624 GCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAG 5683

Qy   5590 CTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAGTGTCTATGC 5649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5684 CTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAGTGTCTATGC 5743

Qy   5650 TCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTGTCACCACTCTGGAGAATGT 5709
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5744 TCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTGTCACCACTCTGGAGAATGT 5803

Qy   5710 CAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACCATTAGCTG 5769
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5804 CAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACCATTAGCTG 5863

Qy   5770 GAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGATGCCGTTCCAGCCAATGGCCA 5829
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   5864 GAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCCAATGGCCA 5923

Qy   5830 GACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACTGGCTTACA 5889
          ||||||||||||||||||||||||||||||||||||||||||||||||||| || |||||
Db   5924 GACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACAGGTTTACA 5983

Qy   5890 ACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTCCCC 5949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5984 ACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTCCCC 6043

Qy   5950 TGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCAC 6009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6044 TGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCAC 6103

Qy   6010 CACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACCGGCTACAT 6069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6104 CACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACCGGCTACAT 6163

Qy   6070 CATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGG 6129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6164 CATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGG 6223

Qy   6130 TGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCAT 6189
          ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   6224 TGTCACAGAGGCTACTATTCCTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCAT 6283

Qy   6190 TGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCT 6249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6284 TGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCT 6343

Qy   6250 TCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTTGGATGTTCC 6309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6344 TCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTTGGATGTTCC 6403
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Qy       6310 TTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGGAAATGGTAT 6369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6404 TTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGGAAATGGTAT 6463

Qy       6370 TCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGATCTTTGAGGA 6429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6464 TCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGATCTTTGAGGA 6523

Qy       6430 ACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCATAGGCCAAG 6489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6524 ACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCATAGGCCAAG 6583

Qy       6490 ACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTCATGGCCCC 6549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6584 ACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTCATGGCCCC 6643

Qy       6550 ATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTGTTGGCACTGATGAAGAACC 6609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6644 ATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTGTTGGCACTGATGAAGAACC 6703

Qy       6610 CTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTCTGACAGGCCTCACCAGAGG 6669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6704 CTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTCTGACAGGCCTCACCAGAGG 6763

Qy       6670 TGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAAGGTTCGGGA 6729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6764 TGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAAGGTTCGGGA 6823

Qy       6730 AGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATGACTC 6789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6824 AGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATGACTC 6883

Qy       6790 GTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTC 6849
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       6884 GTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTC 6943

Qy       6850 TGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTCAGATG 6909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6944 TGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTCAGATG 7003

Qy       6910 TGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGAGAAGTGGGA 6969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7004 TGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGAGAAGTGGGA 7063

Qy       6970 CCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTCTTGGGAACGGAAAAGGAGA 7029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7064 CCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTCTTGGGAACGGAAAAGGAGA 7123

Qy       7030 ATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGATGGGAAGACATACCACGTAGG 7089
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Db       7124 ATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGATGGGAAGACATACCACGTAGG 7183

Qy       7090 AGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTTTGGAGGCCA 7149
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Db       7184 AGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTTTGGAGGCCA 7243

Qy       7150 GCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGGTGAACCCAGTCCCGAAGGCAC 7209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7244 GCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGGTGAACCCAGTCCCGAAGGCAC 7303

Qy       7210 TACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCATCAGAGAACAAACACTAATGT 7269
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Db       7304 TACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCATCAGAGAACAAACACTAATGT 7363

Qy       7270 TAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGGCTGACAGAGAAGATTCCCG 7329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7364 TAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGGCTGACAGAGAAGATTCCCG 7423

Qy       7330 AGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCTCTCTGCCAAGATCCATCTA 7389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7424 AGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCTCTCTGCCAAGATCCATCTA 7483

Qy       7390 AACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTCTTTCTTTCTTAAGCCCTTTGC 7449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7484 AACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTCTTTCTTTCTTAAGCCCTTTGC 7543

Qy       7450 TCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCTTCTCCAAGCATCACCCTGGGA 7509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7544 TCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCTTCTCCAAGCATCACCCTGGGA 7603

Qy       7510 GTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATTGCCTGTTCTGCTTCGAAGTAT 7569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7604 GTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATTGCCTGTTCTGCTTCGAAGTAT 7663

Qy       7570 TCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATTTGGTTTGGGATCAATAGGA 7629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7664 TCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATTTGGTTTGGGATCAATAGGA 7723

Qy       7630 AAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGATATGACCAAAATTTTAAGT 7689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7724 AAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGATATGACCAAAATTTTAAGT 7783

Qy       7690 AGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGTCTGGCCCGCAATACTGTAGGA 7749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7784 AGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGTCTGGCCCGCAATACTGTAGGA 7843

Qy       7750 ACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCACAGTACT 7795
              ||||||||||||||||||||||||||||||||||||||||||||||
Db       7844 ACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCACAGTACT 7889

RESULT 3
AAI57804
ID   AAI57804 standard; cDNA; 8230 BP.
XX
AC   AAI57804;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 7.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US034263.
XX
PR   23-DEC-1999;   99US-00471275.
PR   21-JAN-2000; 2000US-00488725.
PR   25-APR-2000; 2000US-00552317.
PR   20-JUN-2000; 2000US-00598042.
PR   19-JUL-2000; 2000US-00620312.
PR   03-AUG-2000; 2000US-00653450.
PR   14-SEP-2000; 2000US-00662191.
PR   19-OCT-2000; 2000US-00693036.
PR   29-NOV-2000; 2000US-00727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J,  Zhao QA;
PI   Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   P-PSDB; AAM38648.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders such
PT   as central nervous system injuries.
XX
PS   Claim 1; SEQ ID NO 7; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC   encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders. Note: The sequence data for this patent did not form
CC   part of the printed specification
XX
SQ   Sequence 8230 BP; 2209 A; 2153 C; 2013 G; 1855 T; 0 U; 0 Other;

  Query Match             98.4%;  Score 7671.8;  DB 4;  Length 8230;
  Best Local Similarity   98.7%;  Pred. No. 0;
  Matches 7779;  Conservative    0;  Mismatches    7;  Indels   93;  Gaps    1;

Qy         10 CCGGCTGTGCTGCACAGGGGGAGGAGAGGGAACCCCAGGCGCGAGCGGGAAGAGGGGACC 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 CCGGCTGTGCTGCACAGGGGGAGGAGAGGGAACCCCAGGCGCGAGCGGGAAGAGGGGACC 163

Qy         70 TGCAGCCACAACTTCTCTGGTCCTCTGCATCCCTTCTGTCCCTCCACCCGTCCCCTTCCC 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 TGCAGCCACAACTTCTCTGGTCCTCTGCATCCCTTCTGTCCCTCCACCCGTCCCCTTCCC 223

Qy        130 CACCCTCTGGCCCCCACCTTCTTGGAGGCGACAACCCCCGGGAGGCATTAGAAGGGATTT 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 CACCCTCTGGCCCCCACCTTCTTGGAGGCGACAACCCCCGGGAGGCATTAGAAGGGATTT 283

Qy        190 TTCCCGCAGGTTGCGAAGGGAAGCAAACTTGGTGGCAACTTGCCTCCCGGTGCGGGCGTC 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        250 TCTCCCCCACCGTCTCAACATGCTTAGGGGTCCGGGGCCCGGGCTGCTGCTGCTGGCCGT 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 TCTCCCCCACCGTCTCAACATGCTTAGGGGTCCGGGGCCCGGGCTGCTGCTGCTGGCCGT 403

Qy        310 CCTGTGCCTGGGGACAGCGGTGCCCTCCACGGGAGCCTCGAAGAGCAAGAGGCAGGCTCA 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 CCTGTGCCTGGGGACAGCGGTGCCCTCCACGGGAGCCTCGAAGAGCAAGAGGCAGGCTCA 463

Qy        370 GCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCGGTTGTTATGA 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 GCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCGGTTGTTATGA 523

Qy        430 CAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGCAATGCGTT 489
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Db        524 CAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGCAATGCGTT 583

Qy        490 GGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAACCTGAAGCTGA 549
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db        584 GGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAGAGTAAACCTGAAGCTGA 643

Qy        550 AGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACACTTATGAGCG 609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        644 AGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACACTTATGAGCG 703

Qy        610 TCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGGAGAATAAG 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 TCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGGAGAATAAG 763

Qy        670 CTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGGTGACACCTG 729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        764 CTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGGTGACACCTG 823

Qy        730 GAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTGTGTGTGTCTTGGTAATGGAAA 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        824 GAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTGTGTGTGTCTTGGTAATGGAAA 883

Qy        790 AGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTC 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        884 AGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTC 943

Qy        850 CTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTAC 909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        944 CTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTAC 1003

Qy        910 TTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCA 969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 TTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCA 1063

Qy        970 GGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAA 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 GGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAA 1123

Qy       1030 CCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACAC 1089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 CCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACAC 1183

Qy       1090 CTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTGCAGCTGTTTA 1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1184 CTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTGCAGCTGTTTA 1243

Qy       1150 CCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCACTGTGTCACAGACAGTGGTGT 1209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1244 CCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCACTGTGTCACAGACAGTGGTGT 1303

Qy       1210 GGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGGAAATAAGCAAATGCTTTGCAC 1269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1304 GGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGGAAATAAGCAAATGCTTTGCAC 1363

Qy       1270 GTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGTAACCCAGACTTACGGTGGCAA 1329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1364 GTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGTAACCCAGACTTACGGTGGCAA 1423

Qy       1330 CTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAATGGCAGGACGTTCTACTCCTG 1389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1424 CTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAATGGCAGGACGTTCTACTCCTG 1483

Qy       1390 CACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAGCACAACTTCGAATTATGAGCA 1449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1484 CACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAGCACAACTTCGAATTATGAGCA 1543

Qy       1450 GGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTTGGTTCAGACTCGAGGAGGAAA 1509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1544 GGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTTGGTTCAGACTCGAGGAGGAAA 1603

Qy       1510 TTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAACAACCACAATTACACTGATTG 1569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1604 TTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAACAACCACAATTACACTGATTG 1663

Qy       1570 CACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGGGACCACACAGAACTATGATGC 1629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1664 CACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGGGACCACACAGAACTATGATGC 1723

Qy       1630 CGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGAGGAAATCTGCACAACCAATGA 1689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1724 CGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGAGGAAATCTGCACAACCAATGA 1783

Qy       1690 AGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCAGCATGACATGGGTCACATGAT 1749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1784 AGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCAGCATGACATGGGTCACATGAT 1843

Qy       1750 GAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGACATGCATTGCCTACTCGCAGCT 1809
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1844 GAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGACATGCATTGCCTACTCGCAACT 1903
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Qy   1810 TCGAGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATTCCACAAGCG 1869
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Db   1904 TCGAGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATTCCACAAGCG 1963

Qy   1870 TCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGCAGGTGGAA 1929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1964 TCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGCAGGTGGAA 2023

Qy   1930 GTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCAAATTGGAGA 1989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2024 GTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCAAATTGGAGA 2083

Qy   1990 TTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGCCGTGGCAT 2049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2084 TTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGCCGTGGCAT 2143

Qy   2050 TGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCCTGTCGAAGT 2109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2144 TGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCCTGTCGAAGT 2203

Qy   2110 ATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAATGCACCACA 2169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2204 ATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAATGCACCACA 2263

Qy   2170 GCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTAGGCCGTTG 2229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2264 GCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTAGGCCGTTG 2323

Qy   2230 GAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTGAAGCCTGG 2289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2324 GAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTGAAGCCTGG 2383

Qy   2290 TGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAAGTGACTCG 2349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2384 TGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAAGTGACTCG 2443

Qy   2350 CTTTGACTTCACCACCACCAGCACCAGCACACCTGTGACCAGCAACACCGTGACAGGAGA 2409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2444 CTTTGACTTCACCACCACCAGCACCAGCACACCTGTGACCAGCAACACCGTGACAGGAGA 2503

Qy   2410 GACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATCACAGCCAG 2469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2504 GACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATCACAGCCAG 2563

Qy   2470 TAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGGGTGGAATA 2529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2564 TAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGGGTGGAATA 2623

Qy   2530 TGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACAGCCACTTC 2589
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2624 TGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACAGCCACTTC 2683

Qy   2590 TGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTATCAGATATC 2649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2684 TGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTATCAGATATC 2743

Qy   2650 TGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCCTGATGCCCC 2709
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2744 TGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCCTGATGCCCC 2803

Qy   2710 TCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGGAGCAGACC 2769
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2804 TCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGGAGCAGACC 2863

Qy   2770 CCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGTAGCAGCAC 2829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2864 CCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGTAGCAGCAC 2923

Qy   2830 AGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAACCTGGTGT 2889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2924 AGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAACCTGGTGT 2983

Qy   2890 TCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCTGTTGTCAT 2949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2984 TCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCTGTTGTCAT 3043

Qy   2950 TCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGGGACCTGCA 3009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3044 TCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGGGACCTGCA 3103

Qy   3010 GTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAGAGTGCAGT 3069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3104 GTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAGAGTGCAGT 3163

Qy   3070 GACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGGCAGAGGCT 3129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3164 GACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGGCAGAGGCT 3223

Qy   3130 GCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTCACCTATTA 3189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3224 GCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTCACCTATTA 3283

Qy   3190 CTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCTCAACAGAC 3249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3284 CTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCTCAACAGAC 3343

Qy   3250 AACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCTACTGTCCT 3309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3344 AACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCTACTGTCCT 3403

Qy   3310 GGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGTGGGCCTTAC 3369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3404 GGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGTGGGCCTTAC 3463

Qy   3370 CCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTACCCACTGAG 3429
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3464 CCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTACCCACTGAG 3523

Qy   3430 GAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGCAACCAAGA 3489
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3524 GAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGCAACCAAGA 3583

Qy   3490 GAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATTCCACCTTA 3549
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3584 GAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATTCCACCTTA 3643

Qy   3550 CAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCCAAGAATTGG 3609
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3644 CAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCCAAGAATTGG 3703

Qy   3610 TTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTGACTTCAGA 3669
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3704 TTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTGACTTCAGA 3763

Qy   3670 CTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTACACCATCCA 3729
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3764 CTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTACACCATCCA 3823

Qy   3730 AGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTGACACCATT 3789
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3824 AGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTGACACCATT 3883

Qy   3790 GTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTCACAGTCTC 3849
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3884 GTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTCACAGTCTC 3943

Qy   3850 CTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACCCCTACAAA 3909
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3944 CTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACCCCTACAAA 4003

Qy   3910 CGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCCTGCACTTT 3969
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4004 CGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCCTGCACTTT 4063

Qy   3970 TGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAGGATGACAA 4029
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4064 TGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAGGATGACAA 4123

Qy        4030 GGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCACTGACCTGCG 4089
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4124 GGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCACTGACCTGCG 4183

Qy        4090 ATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCCATCCATTGA 4149
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4184 ATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCCATCCATTGA 4243

Qy        4150 TTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGTTGCAGAGTT 4209
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4244 TTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGTTGCAGAGTT 4303

Qy        4210 GTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGGTACAGAATA 4269
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4304 GTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGGTACAGAATA 4363

Qy        4270 TGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGAGGAAGACA 4329
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4364 TGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGAGGAAGACA 4423

Qy        4330 GAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGCCAACTCTTT 4389
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4424 GAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGCCAACTCTTT 4483

Qy        4390 TACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGCCATCATCC 4449
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4484 TACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGCCATCATCC 4543

Qy        4450 CGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAATTCCATCAC 4509
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4544 CGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAATTCCATCAC 4603

Qy        4510 CCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCTTAATGGCAG 4569
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4604 CCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCTTAATGGCAG 4663

Qy        4570 AGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCGAGGGACCT 4629
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4664 AGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCGAGGGACCT 4723

Qy        4630 GGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCCTGCTGTCAC 4689
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4724 GGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCCTGCTGTCAC 4783

Qy        4690 AGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGTCCAGGAGTT 4749
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4784 AGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGTCCAGGAGTT 4843

Qy        4750 CACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGGAGTTGATTA 4809
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4844 CACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGGAGTTGATTA 4903

Qy        4810 TACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGCAAGCCAAT 4869
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4904 TACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGCAAGCCAAT 4963

Qy        4870 TTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTCA 4929
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4964 TTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTCA 5023

Qy        4930 GGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGTTACAGAGT 4989
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5024 GGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGTTACAGAGT 5083

Qy        4990 AACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGGTCCAGATCA 5049
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5084 AACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGGTCCAGATCA 5143

Qy        5050 AACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAGTGTCTATGC 5109
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5144 AACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAGTGTCTATGC 5203

Qy        5110 TCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAACATTGATCG 5169
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5204 TCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAACATTGATCG 5263

Qy        5170 CCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGCTTGGGAAAG 5229
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5264 CCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGCTTGGGAAAG 5323

Qy        5230 CCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGATGGAATCCA 5289
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5324 CCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGATGGAATCCA 5383

Qy        5290 TGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGCCTCAGACC 5349
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5384 TGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGCCTCAGACC 5443

Qy        5350 GGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAGCCAGCCCCT 5409
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5444 GGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAGCCAGCCCCT 5503

Qy        5410 GATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCACTCAGGTCAC 5469
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5504 GATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCACTCAGGTCAC 5563

Qy        5470 ACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGGATATCGAGT 5529
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5564 ACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGGATATCGAGT 5623

Qy        5530 GCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAG 5589
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5624 GCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAG 5683

Qy        5590 CTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAGTGTCTATGC 5649
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5684 CTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAGTGTCTATGC 5743

Qy        5650 TCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTGTCACCACTCTGGAGAATGT 5709
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5744 TCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTGTCACCACTCTGGAGAATGT 5803

Qy        5710 CAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACCATTAGCTG 5769
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5804 CAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACCATTAGCTG 5863

Qy        5770 GAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGATGCCGTTCCAGCCAATGGCCA 5829
               |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        5864 GAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCCAATGGCCA 5923

Qy        5830 GACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACTGGCTTACA 5889
               ||||||||||||||||||||||||||||||||||||||||||||||||||| || |||||
Db        5924 GACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACAGGTTTACA 5983

Qy        5890 ACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTCCCC 5949
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5984 ACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTCCCC 6043

Qy        5950 TGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCAC 6009
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6044 TGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCAC 6103

Qy        6010 CACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACCGGCTACAT 6069
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6104 CACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACCGGCTACAT 6163

Qy        6070 CATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGG 6129
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6164 CATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGG 6223

Qy        6130 TGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCAT 6189
               ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        6224 TGTCACAGAGGCTACTATTCCTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCAT 6283
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y       6190 TGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCT 6249
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6284 TGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCT 6343

y       6250 TCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTTGGATGTTCC 6309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6344 TCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTTGGATGTTCC 6403

y       6310 TTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGGAAATGGTAT 6369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6404 TTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGGAAATGGTAT 6463

y       6370 TCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGATCTTTGAGGA 6429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6464 TCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGATCTTTGAGGA 6523

y       6430 ACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCATAGGCCAAG 6489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6524 ACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCATAGGCCAAG 6583

y       6490 ACCATACCCGCCGAATGT------------------------------------------ 6507
             ||||||||||||||||||
b       6584 ACCATACCCGCCGAATGTAGGTGAGGAAATCCAAATTGGTCACATCCCCAGGGAAGATGT 6643

y       6508 ---------------------------------------------------AGGACAAGA 6516
                                                                ||||||||| 
b       6644 AGACTATCACCTGTACCCACACGGTCCGGGGCTCAATCCAAATGCCTCTACAGGACAAGA 6703

y       6517 AGCTCTCTCTCAGACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCAT 6576
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6704 AGCTCTCTCTCAGACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCAT 6763

y       6577 TTCATGTCATCCTGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTC 6636
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6764 TTCATGTCATCCTGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTC 6823

y       6637 TACCAGTGCCACTCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGC 6696
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6824 TACCAGTGCCACTCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGC 6883

y       6697 ACTGAAAGACCAGCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGT 6756
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6884 ACTGAAAGACCAGCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGT 6943

y       6757 CAACGAAGGCTTGAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCA 6816
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
b       6944 CAACGAAGGCTTGAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCA 7003

y       6817 TTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCA 6876
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       7004 TTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCA 7063

y       6877 GTGCTTAGGCTTTGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAA 6936
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       7064 GTGCTTAGGCTTTGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAA 7123

y       6937 TGGTGTGAACTACAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGAT 6996
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       7124 TGGTGTGAACTACAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGAT 7183

y       6997 GAGCTGCACATGTCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAAC 7056
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       7184 GAGCTGCACATGTCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAAC 7243

y       7057 GTGTTACGATGATGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGG 7116
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       7244 GTGTTACGATGATGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGG 7303

y       7117 TGCCATTTGCTCCTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCG 7176
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       7304 TGCCATTTGCTCCTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCG 7363

y       7177 CAGACCTGGGGGTGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTC 7236
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7364 CAGACCTGGGGGTGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTC 7423

Qy      7237 TCAGAGATACCATCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCC 7296
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7424 TCAGAGATACCATCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCC 7483

Qy      7297 TTTAGATGTACAGGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAG 7356
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7484 TTTAGATGTACAGGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAG 7543

Qy      7357 GAACAAGCATGTCTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGC 7416
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7544 GAACAAGCATGTCTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGC 7603

Qy      7417 TTAGAGTTCTTCTTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCT 7476
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7604 TTAGAGTTCTTCTTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCT 7663

Qy      7477 CAACTCACAGCTTCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGA 7536
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7664 CAACTCACAGCTTCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGA 7723

Qy      7537 GGGCTGCACATTGCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAA 7596
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7724 GGGCTGCACATTGCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAA 7783

Qy      7597 GTGATTCTAAGATTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAA 7656
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7784 GTGATTCTAAGATTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAA 7843

Qy      7657 ATGTTTTGAAATGATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTT 7716
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7844 ATGTTTTGAAATGATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTT 7903

Qy      7717 TCACTTAAGTGTCTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATAT 7776
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7904 TCACTTAAGTGTCTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATAT 7963

Qy      7777 TTTAAATATCCACAGTACT 7795
             |||||||||||||||||||
Db      7964 TTTAAATATCCACAGTACT 7982


RESULT 4
AAI57802
ID   AAI57802 standard; cDNA; 8062 BP.
XX
AC   AAI57802;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 5.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US034263.
XX
PR   23-DEC-1999;   99US-00471275.
PR   21-JAN-2000; 2000US-00488725.
PR   25-APR-2000; 2000US-00552317.
PR   20-JUN-2000; 2000US-00598042.
PR   19-JUL-2000; 2000US-00620312.
PR   03-AUG-2000; 2000US-00653450.
PR   14-SEP-2000; 2000US-00662191.
PR   19-OCT-2000; 2000US-00693036.
PR   29-NOV-2000; 2000US-00727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J,  Zhao QA;
PI   Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   P-PSDB; AAM38646.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders such
PT   as central nervous system injuries.
XX
PS   Claim 1; SEQ ID NO 5; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC   encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders. Note: The sequence data for this patent did not form
CC   part of the printed specification
XX
SQ   Sequence 8062 BP; 2164 A; 2099 C; 1980 G; 1819 T; 0 U; 0 Other;

  Query Match             97.7%;  Score 7614.8;  DB 4;  Length 8062;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches 7704;  Conservative    0;  Mismatches    7;  Indels   75;  Gaps    1;

Qy         10 CCGGCTGTGCTGCACAGGGGGAGGAGAGGGAACCCCAGGCGCGAGCGGGAAGAGGGGACC 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 CCGGCTGTGCTGCACAGGGGGAGGAGAGGGAACCCCAGGCGCGAGCGGGAAGAGGGGACC 163

Qy         70 TGCAGCCACAACTTCTCTGGTCCTCTGCATCCCTTCTGTCCCTCCACCCGTCCCCTTCCC 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 TGCAGCCACAACTTCTCTGGTCCTCTGCATCCCTTCTGTCCCTCCACCCGTCCCCTTCCC 223

Qy        130 CACCCTCTGGCCCCCACCTTCTTGGAGGCGACAACCCCCGGGAGGCATTAGAAGGGATTT 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 CACCCTCTGGCCCCCACCTTCTTGGAGGCGACAACCCCCGGGAGGCATTAGAAGGGATTT 283

Qy        190 TTCCCGCAGGTTGCGAAGGGAAGCAAACTTGGTGGCAACTTGCCTCCCGGTGCGGGCGTC 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 TTCCCGCAGGTTGCGAAGGGAAGCAAACTTGGTGGCAACTTGCCTCCCGGTGCGGGCGTC 343

Qy        250 TCTCCCCCACCGTCTCAACATGCTTAGGGGTCCGGGGCCCGGGCTGCTGCTGCTGGCCGT 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 TCTCCCCCACCGTCTCAACATGCTTAGGGGTCCGGGGCCCGGGCTGCTGCTGCTGGCCGT 403

Qy        310 CCTGTGCCTGGGGACAGCGGTGCCCTCCACGGGAGCCTCGAAGAGCAAGAGGCAGGCTCA 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 CCTGTGCCTGGGGACAGCGGTGCCCTCCACGGGAGCCTCGAAGAGCAAGAGGCAGGCTCA 463

Qy        370 GCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCGGTTGTTATGA 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 GCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCGGTTGTTATGA 523

Qy        430 CAATGGAAAACACTATCAGATAAATCAACAGTGGAGCGGACCTACCTAGGCAATGCGTT 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 CAATGGAAAACACTATCAGATAAATCAACAGTGGAGCGGACCTACCTAGGCAATGCGTT 583

Qy        490 GGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAACCTGAAGCTGA 549
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db        584 GGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAGAGTAAACCTGAAGCTGA 643

Qy        550 AGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGTGACACTTATGAGCG 609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        644 AGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGTGACACTTATGAGCG 703

Qy        610 TCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGGAGAATAAG 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 TCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGGAGAATAAG 763

Qy        670 CTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGGTGACACCTG 729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        764 CTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGGTGACACCTG 823

Qy        730 GAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTGTGTGTGTCTTGGTAATGGAAA 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        824 GAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTGTGTGTGTCTTGGTAATGGAAA 883

Qy        790 AGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTC 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        884 AGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTC 943

Qy        850 CTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTAC 909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        944 CTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTAC 1003

Qy        910 TTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCA 969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 TTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCA 1063

Qy        970 GGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAA 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 GGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCGAGGAAA 1123

Qy       1030 CCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACAC 1089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 CCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACAC 1183

Qy       1090 CTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTGCAGCTGTTTA 1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1184 CTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTGCAGCTGTTTA 1243

Qy       1150 CCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCACTGTGTCACAGACAGTGGTGT 1209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1244 CCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCACTGTGTCACAGACAGTGGTGT 1303

Qy       1210 GGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGGAAATAAGCAAATGCTTTGCAC 1269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1304 GGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGGAAATAAGCAAATGCTTTGCAC 1363

Qy       1270 GTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGTAACCCAGACTTACGGTGGCAA 1329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1364 GTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGTAACCCAGACTTACGGTGGCAA 1423

Qy       1330 CTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAATGGCAGGACGTTCTACTCCTG 1389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1424 CTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAATGGCAGGACGTTCTACTCCTG 1483

Qy       1390 CACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAGCACAACTTCGAATTATGAGCA 1449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1484 CACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAGCACAACTTCGAATTATGAGCA 1543

Qy       1450 GGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTTGGTTCAGACTCGAGGAGGAAA 1509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1544 GGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTTGGTTCAGACTCGAGGAGGAAA 1603

Qy       1510 TTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAACAACCACAATTACACTGATTG 1569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1604 TTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAACAACCACAATTACACTGATTG 1663
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y     1570 CACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGGACCACACAGAACTATGATGC 1629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     1664 CACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGGACCACACAGAACTATGATGC 1723

y     1630 CGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGAGGAAATCTGCACAACCAATGA 1689
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     1724 CGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGAGGAAATCTGCACAACCAATGA 1783

y     1690 AGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCAGCATGACATGGGTCACATGAT 1749
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     1784 AGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCAGCATGACATGGGTCACATGAT 1843

y     1750 GAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGACATGCATTGCCTACTCGCAGCT 1809
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
b     1844 GAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGACATGCATTGCCTACTCGCAACT 1903

y     1810 TCGAGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATTCCACAAGCG 1869
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     1904 TCGAGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATTCCACAAGCG 1963

y     1870 TCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGCAGGTGGAA 1929
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     1964 TCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGCAGGTGGAA 2023

y     1930 GTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCAAATTGGAGA 1989
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     2024 GTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCAAATTGGAGA 2083

y     1990 TTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGCCGTGGCAT 2049
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     2084 TTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGCCGTGGCAT 2143

y     2050 TGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCCTGTCGAAGT 2109
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     2144 TGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCCTGTCGAAGT 2203

y     2110 ATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAATGCACCACA 2169
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     2204 ATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAATGCACCACA 2263

y     2170 GCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTAGGCCGTTG 2229
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     2264 GCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTAGGCCGTTG 2323

y     2230 GAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTGAAGCCTGG 2289
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     2324 GAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTGAAGCCTGG 2383

y     2290 TGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAAGTGACTCG 2349
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     2384 TGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAAGTGACTCG 2443

y     2350 CTTTGACTTCACCACCACCAGCACCAGCACACCTGTGACCAGCAACACCGTGACAGGAGA 2409
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     2444 CTTTGACTTCACCACCACCAGCACCAGCACACCTGTGACCAGCAACACCGTGACAGGAGA 2503

y     2410 GACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATCACAGCCAG 2469
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     2504 GACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATCACAGCCAG 2563

y     2470 TAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGGGTGGAATA 2529
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     2564 TAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGGGTGGAATA 2623

y     2530 TGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACAGCCACTTC 2589
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     2624 TGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACAGCCACTTC 2683

y     2590 TGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTATCAGATATC 2649
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b     2684 TGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTATCAGATATC 2743

y     2650 TGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCCTGATGCCCC 2709
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2744 TGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAACAGCGCCTGATGCCCC 2803

Qy    2710 TCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGGAGCAGACC 2769
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2804 TCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAATTGTTGTTCGCTGGAGCAGACC 2863

Qy    2770 CCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGTAGCAGCAC 2829
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2864 CCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGTAGCAGCAC 2923

Qy    2830 AGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAACCTGGTGT 2889
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2924 AGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAACCTGGTGT 2983

Qy    2890 TCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCTGTTGTCAT 2949
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2984 TCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCTGTTGTCAT 3043

Qy    2950 TCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGGGACCTGCA 3009
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3044 TCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGTGCCCTCTCCCAGGGACCTGCA 3103

Qy    3010 GTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAGAGTGCAGT 3069
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3104 GTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAGAGTGCAGT 3163

Qy    3070 GACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGGCAGAGGCT 3129
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3164 GACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGGCAGAGGCT 3223

Qy    3130 GCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTCACCTATTA 3189
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3224 GCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTCACCTATTA 3283

Qy    3190 CTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCTCAACAGAC 3249
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3284 CTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCTCAACAGAC 3343

Qy    3250 AACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCTACTGTCCT 3309
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3344 AACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCTACTGTCCT 3403

Qy    3310 GGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGTGGGCCTTAC 3369
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3404 GGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGTGGGCCTTAC 3463

Qy    3370 CCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTACCCACTGAG 3429
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3464 CCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTACCCACTGAG 3523

Qy    3430 GAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGCAACCAAGA 3489
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3524 GAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGCAACCAAGA 3583

Qy    3490 GAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATTCCACCTTA 3549
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3584 GAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATTCCACCTTA 3643

Qy    3550 CAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCCAAGAATTGG 3609
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3644 CAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCCAAGAATTGG 3703

Qy    3610 TTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTGACTTCAGA 3669
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3704 TTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGCACCACGAGAAGTGACTTCAGA 3763

Qy    3670 CTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTACACCATCCA 3729
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3764 CTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTACACCATCCA 3823

Qy    3730 AGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTGACACCATT 3789
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3824 AGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTGACACCATT 3883

Qy   3790 GTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTCACAGTCTC 3849
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3884 GTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTCACAGTCTC 3943

Qy   3850 CTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACCCCTACAAA 3909
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3944 CTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACCCCTACAAA 4003

Qy   3910 CGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCCTGCACTTT 3969
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4004 CGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCCTGCACTTT 4063

Qy   3970 TGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAGGATGACAA 4029
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4064 TGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAGGATGACAA 4123

Qy   4030 GGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCACTGACCTGCG 4089
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4124 GGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCCACTGACCTGCG 4183

Qy   4090 ATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCCATCCATTGA 4149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4184 ATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCCATCCATTGA 4243

Qy   4150 TTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGTTGCAGAGTT 4209
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4244 TTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGTTGCAGAGTT 4303

Qy   4210 GTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGGTACAGAATA 4269
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4304 GTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGGTACAGAATA 4363

Qy   4270 TGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGAGGAAGACA 4329
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4364 TGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGAGGAAGACA 4423

Qy   4330 GAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGCCAACTCTTT 4389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4424 GAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGCCAACTCTTT 4483

Qy   4390 TACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGCCATCATCC 4449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4484 TACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGCCATCATCC 4543

Qy   4450 CGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAATTCCATCAC 4509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4544 CGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAATTCCATCAC 4603

Qy   4510 CCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCTTAATGGCAG 4569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4604 CCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCTTAATGGCAG 4663

Qy   4570 AGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCGAGGGACCT 4629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4664 AGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCGAGGGACCT 4723

Qy   4630 GGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCCTGCTGTCAC 4689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4724 GGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCCTGCTGTCAC 4783

Qy   4690 AGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGTCCAGGAGTT 4749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4784 AGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGTCCAGGAGTT 4843

Qy   4750 CACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGGAGTTGATTA 4809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4844 CACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGGAGTTGATTA 4903

Qy   4810 TACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGCAAGCCAAT 4869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4904 TACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGCAAGCCAAT 4963

Qy   4870 TTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTCA 4929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4964 TTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTCA 5023

Qy   4930 GGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGTTACAGAGT 4989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5024 GGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGTTACAGAGT 5083

Qy   4990 AACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGGTCCAGATCA 5049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5084 AACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGGTCCAGATCA 5143

Qy   5050 AACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAGTGTCTATGC 5109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5144 AACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGAGTATGTGGTTAGTGTCTATGC 5203

Qy   5110 TCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAACATTGATCG 5169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5204 TCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAACATTGATCG 5263

Qy   5170 CCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGCTTGGGAAAG 5229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5264 CCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGCTTGGGAAAG 5323

Qy   5230 CCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGATGGAATCCA 5289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5324 CCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGATGGAATCCA 5383

Qy   5290 TGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGCCTCAGACC 5349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5384 TGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGCCTCAGACC 5443

Qy   5350 GGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAGCCAGCCCCT 5409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5444 GGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATATGGAGAGCCAGCCCCT 5503

Qy   5410 GATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCACTCAGGTCAC 5469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5504 GATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCACTCAGGTCAC 5563

Qy   5470 ACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGGATATCGAGT 5529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5564 ACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGGATATCGAGT 5623

Qy   5530 GCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAG 5589
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5624 GCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAG 5683

Qy   5590 CTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAGTGTCTATGC 5649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5684 CTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAGTGTCTATGC 5743

Qy   5650 TCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTGTCACCACTCTGGAGAATGT 5709
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5744 TCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTGTCACCACTCTGGAGAATGT 5803

Qy   5710 CAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACCATTAGCTG 5769
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5804 CAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACCATTAGCTG 5863

Qy   5770 GAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGATGCCGTTCCAGCCAATGGCCA 5829
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   5864 GAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCCAATGGCCA 5923

Qy   5830 GACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACTGGCTTACA 5889
          ||||||||||||||||||||||||||||||||||||||||||||||||||| || |||||
Db   5924 GACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACAGGTTTACA 5983

Qy   5890 ACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTCCCC 5949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5984 ACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTCCCC 6043
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Qy       5950 TGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCAC 6009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6044 TGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCAC 6103

Qy       6010 CACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACCGGCTACAT 6069
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6104 CACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACCGGCTACAT 6163

Qy       6070 CATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGG 6129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6164 CATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGG 6223

Qy       6130 TGTCACAGAGGCTACTATTACTGGCCTGGAACCGGAACCGAATATACAATTTATGTCAT 6189
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       6224 TGTCACAGAGGCTACTATTCCTGGCCTGGAACCGGAACCGAATATACAATTTATGTCAT 6283

Qy       6190 TGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCT 6249
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       6284 TGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAG----------- 6332

Qy       6250 TCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTTGGATGTTCC 6309

Db       6333 ------------------------------------------------------------ 6332

Qy       6310 TTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGGAAATGGTAT 6369
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6333 ----ACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGGAAATGGTAT 6388

Qy       6370 TCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGATCTTTGAGGA 6429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6389 TCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGATCTTTGAGGA 6448

Qy       6430 ACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCATAGGCCAAG 6489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6449 ACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCATAGGCCAAG 6508

Qy       6490 ACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTCATGGGCCCC 6549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6509 ACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTCATGGGCCCC 6568

Qy       6550 ATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTGTTGGCACTGATGAAGAACC 6609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6569 ATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTGTTGGCACTGATGAAGAACC 6628

Qy       6610 CTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTCTGACAGGCCTCACCAGAGG 6669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6629 CTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTCTGACAGGCCTCACCAGAGG 6688

Qy       6670 TGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAAGGTTCGGGA 6729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6689 TGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAAGGTTCGGGA 6748

Qy       6730 AGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATGACTC 6789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6749 AGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATGACTC 6808

Qy       6790 GTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTC 6849
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       6809 GTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTC 6868

Qy       6850 TGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTCAGATG 6909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6869 TGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTCAGATG 6928

Qy       6910 TGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGAGAAGTGGGA 6969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6929 TGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGAGAAGTGGGA 6988

Qy       6970 CCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTCTTGGGAACGGAAAAGGAGA 7029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6989 CCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTCTTGGGAACGGAAAAGGAGA 7048

Qy       7030 ATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGATGGGAAGACATACCACGTAGG 7089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7049 ATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGATGGGAAGACATACCACGTAGG 7108

Qy       7090 AGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTTTGGAGGCCA 7149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7109 AGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTTTGGAGGCCA 7168

Qy       7150 GCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGGTGAACCCAGTCCCGAAGGCAC 7209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7169 GCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGGTGAACCCAGTCCCGAAGGCAC 7228

Qy       7210 TACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCATCAGAGAACAAACACTAATGT 7269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7229 TACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCATCAGAGAACAAACACTAATGT 7288

Qy       7270 TAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGGCTGACAGAGAAGATTCCCG 7329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7289 TAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGGCTGACAGAGAAGATTCCCG 7348

Qy       7330 AGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCTCTCTGCCAAGATCCATCTA 7389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7349 AGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCTCTCTGCCAAGATCCATCTA 7408

Qy       7390 AACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTCTTTCTTTCTTAAGCCCTTTGC 7449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7409 AACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTCTTTCTTTCTTAAGCCCTTTGC 7468

Qy       7450 TCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCTTCTCCAAGCATCACCCTGGGA 7509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7469 TCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCTTCTCCAAGCATCACCCTGGGA 7528

Qy       7510 GTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATTGCCTGTTCTGCTTCGAAGTAT 7569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7529 GTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATTGCCTGTTCTGCTTCGAAGTAT 7588

Qy       7570 TCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATTTGGTTTGGGATCAATAGGA 7629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7589 TCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATTTGGTTTGGGATCAATAGGA 7648

Qy       7630 AAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGATATGACCAAAATTTTAAGT 7689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7649 AAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGATATGACCAAAATTTTAAGT 7708

Qy       7690 AGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGTCTGGCCCGCAATACTGTAGGA 7749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7709 AGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGTCTGGCCCGCAATACTGTAGGA 7768

Qy       7750 ACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCACAGTACT 7795
              ||||||||||||||||||||||||||||||||||||||||||||||
Db       7769 ACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCACAGTACT 7814


RESULT 5
ADB31322
ID   ADB31322 standard; cDNA; 7679 BP.
XX
AC   ADB31322;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Testosterone regulated prostate cancer gene #38.
XX
KW   Human; ss; prostate cancer; cancer; androgen; castration;
KW   anti-androgenic drug; bicalutamide; casodex; testosterone.
XX
OS   Homo sapiens.
XX
PN   US6506607-B1.
XX
PD   14-JAN-2003.
XX
PF   23-DEC-1998;   98US-00220132.
XX
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PR   24-DEC-1997;   97US-0068821P.
PR   25-MAR-1998;   98US-0079303P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Shyjan AW;
XX
DR   WPI; 2003-595981/56.
XX
PT   Determination of whether compound is useful for prostate cancer treatment
PT   comprises measuring expression level of specific nucleic acid sequence in
PT   prostate cancer cell sample in the presence and absence of compound.
XX
PS   Example 1; Col 139-146; 194pp; English.
XX
CC   The invention discloses a method for determining whether a compound can
CC   be used to treat prostate cancer and comprises measuring the expression
CC   level of a nucleic acid in prostate cancer cell sample in the presence
CC   and absence of the compound. Determining whether a compound can be used
CC   to treat prostate cancer comprises identifying the compound as useful for
CC   prostate cancer treatment when the expression level of the nucleic acid
CC   in the presence of the compound is less than the expression level of the
CC   nucleic acid in the absence of the compound. Prostate cancer is usually
CC   tretaed by androgen withdrawal, by castration or through the use of an
CC   anti-androgenic drug. Bicalutamide (casodex) is one such anti-androgenic
CC   compound. The determination whether a selected compound, e.g. an anti-
CC   androgenic compound or testosterone, can be used to treat the prostate
CC   cancer can be made on a patient by patient basis. The sequence presented
CC   is a gene which is more highly expressed in testosterone treated prostate
CC   cancer cells than the untreated cells.
XX
SQ   Sequence 7679 BP; 2081 A; 1981 C; 1862 G; 1755 T; 0 U; 0 Other;

  Query Match             95.2%;  Score 7423;  DB 9;  Length 7679;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7432;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy        349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy        409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy        469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
              |||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy        529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

Qy        589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

Qy        649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy        709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy        769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480

Qy        829 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 540

Qy        889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy        949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

Qy       1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy       1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy       1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy       1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG 1248
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db        841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGTTGAAGACACAAGG 900

Qy       1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy       1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy       1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy       1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy       1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy       1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy       1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy       1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy       1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy       1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db       1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy       1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy       1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy       1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

y    2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

y    2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

y    2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

y    2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

y    2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

y    2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

y    2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

y    2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

y    2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

y    2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

y    2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

y    2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

y    2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

y    2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

y    2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

y    2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

Qy   2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

Qy   3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy   3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy   3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy   3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy   3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy   3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy   3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   3061 TGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy   3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy   3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy   3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy   3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy   3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy   3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy   3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy   3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600

Qy   3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy   4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy   4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy   4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840
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Qy       4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy       4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy       4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy       4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy       4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy       4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy       4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy       4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4320

Qy       4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy       4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy       4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy       4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy       4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

Qy       4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

Qy       5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy       5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800

Qy       5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy       5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy       5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

Qy       5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy       5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy       5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy       5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy       5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy       5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy       5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy       5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy       5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5461 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5520

Qy       5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
              |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db       5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

Qy       5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

Qy       5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy       6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy       6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

Qy       6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

Qy       6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy       6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy       6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

y       6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

y       6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

y       6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6181 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

y       6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300

y       6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360

y       6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

y       6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
             |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
b       6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

y       6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

y       6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

y       6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

y       7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6661 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 6720

y       7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

y       7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6781 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840

Qy      7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6841 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 6900

Qy      7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960

Qy      7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

Qy      7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080

Qy      7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

Qy      7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

Qy      7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260

Qy      7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

Qy      7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy      7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440

Qy      7789 CAGTACT 7795
             |||||||
Db      7441 CAGTACT 7447


RESULT 6
AAF21131
ID   AAF21131 standard; DNA; 7680 BP.
XX
AC   AAF21131;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human low adenosine antisense oligonucleotide related sequence #2698.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US008020.
XX
PR   06-APR-1999;   99US-0127958P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not trigger
PT   adenosine receptors during metabolism, useful e.g. for treating cancers
PT   and respiratory obstructions.
XX
PS   Disclosure; Page 1026-1028; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC   surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention
XX
SQ   Sequence 7680 BP; 2081 A; 1981 C; 1862 G; 1756 T; 0 U; 0 Other;

  Query Match             95.2%;  Score 7423;  DB 3;  Length 7680;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7432;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy    409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy    469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
          |||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db    121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy    529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

Qy    589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

Qy    649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy    709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy    769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480

Qy    829 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 540

Qy    889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy    949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

Qy   1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy   1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy   1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy   1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGATGCAGTGGCTGAAGACACAAGG 1248
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGATGCAGTGGTTGAAGACACAAGG 900

Qy   1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy   1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy   1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy   1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy   1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy   1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy   1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy   1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy   1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy   1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy   1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy   1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy   1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680
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Qy        2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy        2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy        2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy        2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy        2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy        2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy        2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy        2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

Qy        2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

Qy        2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy        2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

Qy        2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy        2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy        2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

Qy        2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

Qy        2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

Qy        2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

Qy        3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy        3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy        3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy        3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy        3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy        3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
               |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy        3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
               ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        3061 TGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy        3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy        3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
               |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db        3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy        3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy        3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy        3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy        3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy        3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy        3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3541 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600

Qy        3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy        4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy        4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy        4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy        4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy   4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy   4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy   4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy   4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy   4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy   4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy   4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4320

Qy   4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy   4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy   4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
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Db   4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy   4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy   4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

Qy   4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy   5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
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Db   4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800

Qy   5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy   5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy   5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980
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Qy   5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
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Db   4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy   5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
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Db   5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy   5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy   5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
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Db   5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy   5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy   5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy   5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy   5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
          ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy   5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5520

Qy   5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
          |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db   5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

Qy   5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

Qy   5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy   6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy   6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

Qy   6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

Qy   6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy   6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy   6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060
```

```
Qy       6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy       6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

Qy       6529 GACAACCATCTCATGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6181 GACAACCATCTCATGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

Qy       6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300

Qy       6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360

Qy       6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

Qy       6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db       6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

Qy       6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

Qy       6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

Qy       6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

Qy       7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6661 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 6720

Qy       7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

Qy       7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6781 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840

Qy       7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6841 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 6900

Qy       7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960

Qy       7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

Qy       7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080

Qy       7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

Qy       7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

Qy       7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260

Qy       7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

Qy       7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy       7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440

Qy       7789 CAGTACT 7795
              |||||||
Db       7441 CAGTACT 7447


RESULT 7
ABA82689
ID   ABA82689 standard; DNA; 7680 BP.
XX
AC   ABA82689;
XX
DT   25-JAN-2002  (first entry)
XX
DE   Fibronectin gene SEQ ID NO:75.
XX
KW   Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3;
KW   sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
KW   antisense therapy; vaccine; bone disorder; Paget's disease; sclerostosis;
KW   osteomalacia; fibrous dysplasia; ds.
XX
OS   Homo sapiens.
XX
PN   WO200177327-A1.
XX
PD   18-OCT-2001.
XX
PF   21-JUN-2000; 2000WO-US016951.
XX
PR   05-APR-2000; 2000US-00543771.
PR   05-APR-2000; 2000US-00544398.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Carulli JP,  Little RD,  Recker RR,  Johnson ML;
XX
DR   WPI; 2001-657171/75.
XX
PT   New high bone mass (HBM) and Zmax1 genes and proteins useful for
PT   modulating bone mass for the treatment of e.g. osteoporosis.
XX
PS   Claim 79; Page 376-378; 443pp; English.
XX
CC   The present invention describes the human Zmax1 gene and the high bone
CC   mass (HBM) gene,which are found on chromosome 11q13.3. The Zmax1 and HBM
CC   genes have osteopathic activities. The genes can be used in gene therapy,
CC   antisense therapy and in the production of vaccines. They can be used in
CC   the diagnosis and treatment of bone disorders including osteoporosis,
CC   Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.
CC   ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in
CC   the exemplification of the present invention
XX
SQ   Sequence 7680 BP; 2081 A; 1981 C; 1862 G; 1756 T; 0 U; 0 Other;

  Query Match             95.2%;  Score 7423;  DB 5;  Length 7680;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7432;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy        349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy        409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy        469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
              |||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy        529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

Qy        589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

Qy        649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy        709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy        769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480

Qy        829 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 540

Qy        889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy        949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

Qy       1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy       1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy       1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy       1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGATGCAGTGGCTGAAGACACAAGG 1248
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGATGCAGTGGTTGAAGACACAAGG 900

Qy       1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy       1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy       1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy       1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy       1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy       1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy       1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy       1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy       1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy       1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db       1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy       1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy       1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy       1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy       2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy       2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy       2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy       2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy       2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy       2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy       2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy       2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160
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Qy   2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

Qy   2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy   2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

Qy   2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy   2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy   2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

Qy   2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

Qy   2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

Qy   2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

Qy   3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy   3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy   3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy   3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy   3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy   3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy   3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   3061 TGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy   3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy   3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy   3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy   3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy   3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy   3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
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Db   3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy   3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy   3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy   4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy   4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy   4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
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Db   3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy   4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy   4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy   4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy   4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
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Db   4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy   4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy   4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy   4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy   4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4320

Qy   4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy       4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy       4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy       4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy       4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

Qy       4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

Qy       5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy       5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800

Qy       5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy       5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy       5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

Qy       5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy       5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy       5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy       5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
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Db       5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy       5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy       5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy       5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy       5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy       5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
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Db       5461 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5520

Qy       5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
              |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db       5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

Qy       5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

Qy       5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy       6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy       6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
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Db       5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

Qy       6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

Qy       6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy       6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy       6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy       6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy       6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

Qy       6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6181 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

Qy       6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300

Qy       6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360

Qy       6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

Qy       6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db       6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

Qy       6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540
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y       6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
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b       6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

y       6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

y       7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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y       7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

y       7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6781 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840

y       7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6841 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 6900

y       7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960

y       7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

y       7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080

y       7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

y       7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

y       7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260

y       7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

y       7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

y       7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440

y       7789 CAGTACT 7795
             |||||||
b       7441 CAGTACT 7447

RESULT 8
ABL67540
ID   ABL67540 standard; DNA; 7680 BP.
XX
AC   ABL67540;
XX
DT   15-MAY-2002  (first entry)
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XX
DE   Thyroid cancer related gene sequence SEQ ID NO:5877.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200194629-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US010838.
XX
PR   05-JUN-2000; 2000US-0209473P.
PR   05-JUN-2000; 2000US-0209531P.
PR   18-SEP-2000; 2000US-0233133P.
PR   18-SEP-2000; 2000US-0233617P.
PR   20-SEP-2000; 2000US-0234009P.
PR   20-SEP-2000; 2000US-0234034P.
PR   20-SEP-2000; 2000US-0234052P.
PR   22-SEP-2000; 2000US-0234509P.
PR   22-SEP-2000; 2000US-0234567P.
PR   25-SEP-2000; 2000US-0234923P.
PR   25-SEP-2000; 2000US-0234924P.
PR   25-SEP-2000; 2000US-0235077P.
PR   25-SEP-2000; 2000US-0235082P.
PR   25-SEP-2000; 2000US-0235134P.
PR   25-SEP-2000; 2000US-0235280P.
PR   26-SEP-2000; 2000US-0235637P.
PR   26-SEP-2000; 2000US-0235638P.
PR   27-SEP-2000; 2000US-0235711P.
PR   27-SEP-2000; 2000US-0235720P.
PR   27-SEP-2000; 2000US-0235840P.
PR   27-SEP-2000; 2000US-0235863P.
PR   28-SEP-2000; 2000US-0236028P.
PR   28-SEP-2000; 2000US-0236032P.
PR   28-SEP-2000; 2000US-0236033P.
PR   28-SEP-2000; 2000US-0236034P.
PR   28-SEP-2000; 2000US-0236109P.
PR   28-SEP-2000; 2000US-0236111P.
PR   29-SEP-2000; 2000US-0236842P.
PR   29-SEP-2000; 2000US-0236891P.
PR   02-OCT-2000; 2000US-0237172P.
PR   02-OCT-2000; 2000US-0237173P.
PR   02-OCT-2000; 2000US-0237278P.
PR   02-OCT-2000; 2000US-0237294P.
PR   02-OCT-2000; 2000US-0237295P.
PR   02-OCT-2000; 2000US-0237316P.
PR   03-OCT-2000; 2000US-0237425P.
PR   03-OCT-2000; 2000US-0237598P.
PR   03-OCT-2000; 2000US-0237604P.
PR   03-OCT-2000; 2000US-0237606P.
PR   03-OCT-2000; 2000US-0237608P.
PR   01-NOV-2000; 2000US-0244867P.
PR   01-NOV-2000; 2000US-0245084P.
XX
PA   (AVAL-) AVALON PHARM.
XX
PI   Young PE,  Augustus M,  Carter KC,  Ebner R,  Endress G,  Horrigan S;
PI   Soppet DR,  Weaver Z;
XX
DR   WPI; 2002-188264/24.
XX
PT   Screening for anti-neoplastic agent involves exposing cells to a chemical
PT   agent to be tested for anti-neoplastic activity, and determining a change
PT   in expression of a gene of a signature gene set.
XX
PS   Claim 1; SEQ ID NO 5877; 44pp; English.
XX
CC   The present invention describes a method (M1) for screening for an anti-
CC   neoplastic agent. The method involves exposing cells to a chemical agent
CC   to be tested for anti-neoplastic activity, determining a change in
CC   expression of at least one gene (I) of a signature gene set, where (I)
CC   comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC   to ABL70110), or is at least 95% identical to (S), where a change in
CC   expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC   activity and can be used in gene therapy. M1 can be used for screening an
CC   anti-neoplastic agent, and can be used for producing a product which is
CC   the data collected with respect to the anti-neoplastic agent as a result
CC   of M1, and the data is sufficient to convey the chemical structure and/or
CC   properties of the agent. M1 can be used in the treatment of cancer such
CC   as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC   prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC   cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC   cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC   tumour
XX
SQ   Sequence 7680 BP; 2081 A; 1981 C; 1862 G; 1756 T; 0 U; 0 Other;

  Query Match             95.2%;  Score 7423;  DB 6;  Length 7680;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7432;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy        349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy        409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy        469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
              |||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy        529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

Qy        589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

Qy        649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy        709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy        769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480

Qy        829 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 540

Qy        889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy        949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

Qy       1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy       1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy       1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy       1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG 1248
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db        841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGTTGAAGACACAAGG 900

Qy       1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy       1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy       1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy       1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy       1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy       1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy       1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy       1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy       1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy       1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db       1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy       1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy       1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy       1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy       2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy       2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy       2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860
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y    2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

y    2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

y    2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

y    2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

y    2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

y    2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

y    2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

y    2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

y    2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

y    2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

y    2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

y    2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b    2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

y    2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

y    2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

Qy   3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy   3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy   3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy   3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940
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Qy   3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy   3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy   3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   3061 TGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy   3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
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Db   3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy   3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy   3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy   3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy   3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy   3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy   3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy   3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600

Qy   3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy   4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy   4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy   4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy   4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy   4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy   4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy   4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy        4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy        4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy        4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy        4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4261 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4320

Qy        4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy        4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy        4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy        4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy        4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

Qy        4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

Qy        5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy        5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800

Qy        5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy        5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy        5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

Qy        5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy        5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy        5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy        5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy        5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy        5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy        5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy        5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
               ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy        5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5461 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5520

Qy        5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
               |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db        5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

Qy        5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

Qy        5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy        6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy        6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

Qy        6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

Qy        6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy        6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy        6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy        6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy        6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

Qy        6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6181 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240
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y        6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300

y        6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360

y        6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

y        6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
b        6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

y        6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

y        6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

y        6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

y        7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        6661 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 6720

y        7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

y        7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        6781 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840

y        7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        6841 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 6900

y        7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960

y        7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

y        7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080

y        7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

y        7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

y        7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260

y        7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320
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Qy       7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy       7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440

Qy       7789 CAGTACT 7795
              |||||||
Db       7441 CAGTACT 7447


RESULT 9
ABT11082
ID   ABT11082 standard; cDNA; 7680 BP.
XX
AC   ABT11082;
XX
DT   04-DEC-2002  (first entry)
XX
DE   Human breast cancer associated coding sequence SEQ ID NO: 1216.
XX
KW   Human; breast specific gene; breast cancer; differential expression;
KW   cytostatic; gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200259271-A2.
XX
PD   01-AUG-2002.
XX
PF   25-JAN-2002; 2002WO-US002176.
XX
PR   25-JAN-2001; 2001US-0263757P.
PR   25-APR-2001; 2001US-0286090P.
PR   23-MAY-2001; 2001US-0292517P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Orr MS,  Nation M,  Diggans JC,  Zeng W;
XX
DR   WPI; 2002-674803/72.
XX
PT   Diagnosing breast cancer in a patient comprises detecting the level of
PT   gene expression in cell or tissue samples, where a differential gene
PT   expression is indicative of breast cancer.
XX
PS   Claim 1; SEQ ID NO 1216; 260pp + Sequence Listing; English.
XX
CC   The present invention relates to methods of diagnosing breast cancer in a
CC   patient, which comprise detecting the level of expression in a tissue
CC   sample of two or more genes selected from those shown in ABT09867-
CC   ABT11112, where a differential expression of the genes indicates breast
CC   cancer. The methods are useful in diagnosing, treating, detecting the
CC   progression, and in monitoring treatment of breast cancer in patients.
CC   The methods are also useful as a screening tool for agents that modulate
CC   the onset or progression of breast cancer. The breast cancer genes may be
CC   used as diagnostic markers for the prediction or identification of the
CC   malignant state of breast tissue, for confirming the type and progression
CC   of cancer, and for drug screening and assays. The present sequence is a
CC   coding sequence of the invention. Note: The sequence data for this patent
CC   did not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub.published_pct_sequences
XX
SQ   Sequence 7680 BP; 2081 A; 1981 C; 1862 G; 1756 T; 0 U; 0 Other;

  Query Match             95.2%;  Score 7423;  DB 6;  Length 7680;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7432;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy        349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy    409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy    469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
          |||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db    121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy    529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

Qy    589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

Qy    649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy    709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy    769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480

Qy    829 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 540

Qy    889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy    949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

Qy   1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy   1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy   1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy   1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG 1248
          |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db    841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGTTGAAGACACAAGG 900

Qy   1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy   1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy   1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
          |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy   1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy   1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy   1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy   1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy   1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy   1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy   1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy   1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy   1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy   1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy   2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy   2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy   2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy   2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy   2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy   2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy   2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy   2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

Qy   2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220
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y  2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b  2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

y  2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b  2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

y  2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b  2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

y  2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b  2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

y  2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b  2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

y  2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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y  2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b  2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

y  2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
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b  2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

y  3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b  2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

y  3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b  2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

y  3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b  2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

y  3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b  2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

y  3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b  2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

y  3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
        |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
b  3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

y  3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
        ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
b  3061 TGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

y  3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b  3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

y  3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
        |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
b  3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

y  3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b  3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300
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Qy  3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
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Db  3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy  3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy  3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy  3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy  3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600

Qy  3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy  4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy  4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy  4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy  4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy  4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy  4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy  4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy  4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy  4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy  4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy  4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
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Db  4261 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4320

Qy  4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy  4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy        4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy        4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy        4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

Qy        4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

Qy        5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy        5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800

Qy        5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy        5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy        5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

Qy        5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy        5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy        5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy        5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy        5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy        5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy        5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy        5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
               ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy        5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5461 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5520

Qy        5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
               |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db        5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

Qy        5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

Qy        5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy        6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy        6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

Qy        6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

Qy        6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy        6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy        6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy        6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy        6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

Qy        6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6181 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

Qy        6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300

Qy        6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360

Qy        6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

Qy        6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
               |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db        6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

Qy        6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

Qy        6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600
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Qy       6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

Qy       7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6661 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 6720

Qy       7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

Qy       7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6781 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840

Qy       7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6841 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 6900

Qy       7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960

Qy       7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

Qy       7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080

Qy       7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

Qy       7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

Qy       7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260

Qy       7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

Qy       7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy       7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440

Qy       7789 CAGTACT 7795
              |||||||
Db       7441 CAGTACT 7447


RESULT 10
ABZ96825
ID   ABZ96825 standard; DNA; 7680 BP.
XX
AC   ABZ96825;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human nucleic acid sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 12067; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 7680 BP; 2081 A; 1981 C; 1862 G; 1756 T; 0 U; 0 Other;

  Query Match             95.2%;  Score 7423;  DB 7;  Length 7680;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7432;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy        349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy        409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy        469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
              |||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy        529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240
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Qy    589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

Qy    649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy    709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy    769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480

Qy    829 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 540

Qy    889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy    949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

Qy   1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy   1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy   1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy   1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG 1248
          |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db    841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGTTGAAGACACAAGG 900

Qy   1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy   1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy   1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy   1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy   1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy   1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy   1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy   1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy   1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy   1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy   1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy   1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy   1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy   2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy   2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy   2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy   2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy   2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy   2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy   2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy   2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

Qy   2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

Qy   2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy   2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

Qy   2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy   2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy    2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

Qy    2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

Qy    2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

Qy    2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

Qy    3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy    3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy    3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy    3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy    3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy    3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
           |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy    3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
           ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    3061 TGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy    3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy    3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
           |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db    3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy    3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy    3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy    3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy    3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy    3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy    3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3541 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600

Qy    3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy    4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy    4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy    4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy    4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy    4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy    4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy    4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy    4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy    4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy    4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy    4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4261 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4320

Qy    4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy    4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy    4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy    4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy    4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620
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Qy          4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

Qy          5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy          5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800

Qy          5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy          5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy          5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

Qy          5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
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Db          4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy          5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy          5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy          5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy          5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy          5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy          5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy          5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
                 ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db          5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy          5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5461 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5520

Qy          5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
                 |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db          5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

Qy          5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

Qy          5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy          6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy          6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

Qy          6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

Qy          6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy          6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy          6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy          6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy          6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

Qy          6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6181 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

Qy          6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300

Qy          6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360

Qy          6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

Qy          6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
                 |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db          6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

Qy          6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

Qy          6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

Qy          6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

Qy          7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6661 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 6720

Qy          7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

Qy          7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        6781 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840

Qy        7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        6841 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 6900

Qy        7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960

Qy        7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

Qy        7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080

Qy        7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

Qy        7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

Qy        7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260

Qy        7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

Qy        7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy        7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440

Qy        7789 CAGTACT 7795
               |||||||
Db        7441 CAGTACT 7447


RESULT 11
ACF03878
ID   ACF03878 standard; cDNA; 7680 BP.
XX
AC   ACF03878;
XX
DT   18-SEP-2003  (first entry)
XX
DE   Human fibronectin encoding cDNA SEQ ID NO:9.
XX
KW   Human; integrin alpha4beta1; fibronectin; integrin alpha 4; VCAM;
KW   integrin beta 1; vascular cell adhesion molecule; angiogenesis;
KW   integrin alpha4beta1 binding inhibitor; angiogenesis inhibitor;
KW   cytostatic; ophthalmological; antirheumatic; antiarthritic; cancer;
KW   antiinflammatory; osteopathic; dermatological; gene therapy; psoriasis;
KW   pathological condition; diabetic retinopathy; macular degeneration;
KW   neovascularisation; rheumatoid arthritis; osteoarthritis; skin cancer;
KW   endothelial progenitor cell; wound healing; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003019136-A2.
XX
PD   06-MAR-2003.
XX
PF   01-AUG-2002; 2002WO-US024573.
XX
PR   06-AUG-2001; 2001US-0310645P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Varner JA;
XX
DR   WPI; 2003-278690/27.
DR   P-PSDB; ABR81866.
XX
PT   Inhibiting angiogenesis in a tissue, useful for treating cancer,
PT   arthritis, retinopathy, psoriasis, by providing a tissue and an agent
PT   that inhibits specific binding of integrin alpha-4beta-1 to an integrin
PT   alpha-4beta-1 ligand.
XX
PS   Disclosure; Fig 17; 177pp; English.
XX
CC   The present invention describes a method for inhibiting angiogenesis in a
CC   tissue comprising providing a tissue and an agent that inhibits specific
CC   binding of integrin alpha4beta1 to an integrin alpha4beta1 ligand, and
CC   treating the tissue with the agent under conditions where the specific
CC   binding of the alpha4beta1 to the ligand is inhibited and a treated
CC   tissue is produced. Angiogenesis in the treated tissue is inhibited. Also
CC   described: (1) inhibiting endothelial cell adhesion or migration; (2)
CC   detecting angiogenesis in a tissue; (3) screening a test compound; (4)
CC   isolating endothelial progenitor cells from a tissue; and (5) reducing
CC   symptoms associated with cancer in a subject, or a pathological condition
CC   is an ocular or skin tissue. An integrin alpha4beta1 binding inhibitor
CC   has cytostatic, ophthalmological, antirheumatic, antiarthritic,
CC   antiinflammatory, osteopathic and dermatological activities, and can be
CC   used in gene therapy. The methods are useful for treating cancer, and
CC   other pathological condition, such as diabetic retinopathy, macular
CC   degeneration by neovascularisation, rheumatoid arthritis, osteoarthritis,
CC   psoriasis or skin cancer. The methods are also useful in isolating
CC   endothelial progenitor cells, and in determining the mechanisms that
CC   underlie angiogenesis, development, wound healing and the function of the
CC   female reproductive system. The present sequence is used in the
CC   exemplification of the present invention
XX
SQ   Sequence 7680 BP; 2081 A; 1981 C; 1862 G; 1756 T; 0 U; 0 Other;

  Query Match             95.2%;  Score 7423;  DB 7;  Length 7680;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7432;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy        349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy        409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy        469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
              |||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy        529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

Qy        589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

Qy        649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy        709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420
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Qy    769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480

Qy    829 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 540

Qy    889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy    949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

Qy   1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy   1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy   1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy   1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGATGCAGTGGCTGAAGACACAAGG 1248
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGATGCAGTGGTTGAAGACACAAGG 900

Qy   1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy   1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy   1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy   1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy   1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy   1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy   1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy   1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy   1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy   1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy   1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy   1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy   1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy   2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy   2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy   2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy   2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy   2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy   2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy   2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy   2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

Qy   2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

Qy   2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy   2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

Qy   2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy   2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy   2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

Qy   2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

Qy   2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

Qy   2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

Qy   3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy   3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy   3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy   3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy   3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy   3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy   3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   3061 TGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy   3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy   3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy   3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy   3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy   3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy   3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy   3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy   3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600

Qy   3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy   4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy   4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy   4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy   4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy   4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy   4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy   4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy   4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy   4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy   4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy   4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4320

Qy   4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy   4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy   4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy   4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy   4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

Qy   4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

Qy   5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy   5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800
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Qy        5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy        5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy        5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

Qy        5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy        5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy        5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy        5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy        5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy        5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy        5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy        5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
               ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy        5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5461 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5520

Qy        5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
               |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db        5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

Qy        5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

Qy        5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy        6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy        6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

Qy        6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

Qy        6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy        6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy        6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy        6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy        6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

Qy        6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6181 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

Qy        6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300

Qy        6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360

Qy        6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

Qy        6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
               |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db        6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

Qy        6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

Qy        6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

Qy        6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

Qy        7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6661 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 6720

Qy        7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

Qy        7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6781 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840

Qy        7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6841 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 6900

Qy        7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960

Qy        7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

Qy       7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080

Qy       7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

Qy       7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

Qy       7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260

Qy       7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

Qy       7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy       7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440

Qy       7789 CAGTACT 7795
              |||||||
Db       7441 CAGTACT 7447


RESULT 12
ABX10391
ID   ABX10391 standard; DNA; 7680 BP.
XX
AC   ABX10391;
XX
DT   28-JAN-2003  (first entry)
XX
DE   DNA encoding protein differentially regulated in prostate cancer #60.
XX
KW   Prostate cancer; gene expression; differential regulation;
KW   molecular marker; drug target; cancer detection; cancer diagnosis;
KW   cancer staging; cancer grading; cancer assessing; cancer monitoring;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200281638-A2.
XX
PD   17-OCT-2002.
XX
PF   08-APR-2002; 2002WO-US010824.
XX
PR   06-APR-2001; 2001US-0281731P.
PR   06-APR-2001; 2001US-0281732P.
XX
PA   (ORIG-) ORIGENE TECHNOLOGIES INC.
XX
PI   Sun Z,  Jay G;
XX
DR   WPI; 2003-058520/05.
DR   P-PSDB; ABU07486.
XX
PT   Novel genes which are differentially regulated in prostate cancer, useful
PT   for diagnosing prostate cancer in prostate tissue sample and assessing
PT   therapeutic or preventive intervention in prostate cancer patients.
XX
PS   Claim 1; Page 136-139; 416pp; English.
XX
CC   The invention describes genes (I) which are differentially regulated in
CC   prostate cancer. (I) Is useful for diagnosing a prostate cancer in a
CC   sample comprising prostate tissue, which involves determining the number
CC   of target genes which are differentially-regulated in the sample, where
CC   the number is indicative of the probability that the sample comprises
CC   prostate cancer. (I) Is useful for assessing a therapeutic or preventive
CC   intervention in a subject having a prostate cancer, which involves
CC   determining the expression levels in a sample comprising prostate tissue
CC   of target genes which are differentially-regulated in prostate cancer.
CC   Preferably, the expression levels of at least 10 genes are determined.
CC   (I) is also useful for identifying agents that modulate a biological
CC   activity of a polypeptide differentially-regulated in prostate cancer
CC   cells, which involves contacting a polypeptide differentially-regulated
CC   in prostate cancer cells with a test agent under conditions effective for
CC   the test agent to modulate a biological activity of the polypeptide, and
CC   determining whether the test agent modulates the biological activity. (I)
CC   is useful as molecular markers, as drug targets, and for detecting,
CC   diagnosing, staging, grading, assessing, monitoring, prognosticating,
CC   preventing or treating, determining predisposition to diseases and
CC   conditions especially relating to prostate cancer. (I) and its expression
CC   products are used in the diagnostic test to assay for presence of cancer
CC   e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
CC   blood etc. (I) is useful for assessing cancer e.g., to determine the type
CC   of cancer, its stage of development, the nature of genetic defect, etc.
CC   The polypeptide encoded by (I) can be used as target for therapy or drug
CC   discovery. (I) can also be used for expressing the polypeptide and thus
CC   for searching specific binding partners of the polypeptide. (I) is useful
CC   in therapeutic applications to treat prostate cancer. The identification
CC   of specific genes, and groups of genes, expressed in pathways
CC   physiologically relevant to prostate cancer permits the definition of
CC   functional and disease pathways and the delineation of targets in these
CC   pathways which are useful in diagnostic, therapeutic, and clinical
CC   applications. This sequence encodes a protein diferentially regulated in
CC   prostate cancer
XX
SQ   Sequence 7680 BP; 2081 A; 1981 C; 1862 G; 1756 T; 0 U; 0 Other;

  Query Match             95.2%;  Score 7423;  DB 7;  Length 7680;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7432;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy        349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy        409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy        469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
              ||||||||||| |||| |||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy        529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

Qy        589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

Qy        649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy        709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy        769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480
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Qy        829 TGATCATGCTGCTGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGATCATGCTGCTGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 540

Qy        889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy        949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

Qy       1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy       1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy       1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy       1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG 1248
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db        841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGTTGAAGACACAAGG 900

Qy       1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy       1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy       1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy       1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy       1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy       1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy       1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy       1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy       1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy       1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db       1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy       1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy       1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy       1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy       2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy       2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy       2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy       2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy       2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy       2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy       2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy       2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

Qy       2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

Qy       2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy       2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

Qy       2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy       2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy       2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

Qy       2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

Qy       2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

Qy       2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

Qy          3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy          3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy          3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy          3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy          3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy          3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
                 |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db          3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy          3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
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Db          3061 TGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy          3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy          3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
                 |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db          3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy          3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
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Db          3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy          3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy          3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy          3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy          3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
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Db          3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy          3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
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Db          3541 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600

Qy          3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy          4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
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Db          3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy          4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy          4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy          4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy          4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy          4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy          4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy          4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy          4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy          4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy          4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4261 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4320

Qy          4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy          4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy          4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy          4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy          4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

Qy          4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

Qy          5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy          5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800

Qy          5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860
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Qy        5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy        5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

Qy        5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy        5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy        5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy        5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy        5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy        5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy        5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy        5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
               ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy        5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5461 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5520

Qy        5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
               |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db        5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

Qy        5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

Qy        5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy        6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy        6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

Qy        6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

Qy        6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940
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Qy        6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy        6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy        6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy        6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

Qy        6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6181 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

Qy        6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300

Qy        6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360

Qy        6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

Qy        6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
               |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db        6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

Qy        6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

Qy        6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

Qy        6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

Qy        7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6661 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 6720

Qy        7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

Qy        7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6781 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840

Qy        7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6841 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 6900

Qy        7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960

Qy        7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

Qy        7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080

Qy         7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

Qy         7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

Qy         7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260

Qy         7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

Qy         7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy         7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440

Qy         7789 CAGTACT 7795
                |||||||
Db         7441 CAGTACT 7447


RESULT 13
ACC46009
ID   ACC46009 standard; DNA; 7680 BP.
XX
AC   ACC46009;
XX
DT   02-JUN-2003  (first entry)
XX
DE   Human fibronectin gene FN.
XX
KW   Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;
KW   gene therapy; bone density modulation; bone strength; trabecular number;
KW   bone size; bone tissue connectivity; bone disease; osteoporosis;
KW   osteomalacia; rickets; Paget's disease; neoplasm of the bone; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200292764-A2.
XX
PD   21-NOV-2002.
XX
PF   13-MAY-2002; 2002WO-US014876.
XX
PR   11-MAY-2001; 2001US-0290071P.
PR   17-MAY-2001; 2001US-0291311P.
PR   01-FEB-2002; 2002US-0353058P.
PR   04-MAR-2002; 2002US-0361293P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
PA   (AMHP ) WYETH.
XX
PI   Babij P,  Bex FJ,  Yaworsky PJ,  Bodine PV;
XX
DR   WPI; 2003-129278/12.
XX
PT   New transgenic animals (e.g. mice), useful as models for studying bone
PT   density modulation, developing drugs for treating or preventing bone
PT   diseases (e.g. osteoporosis), or diagnosing diseases characterized by
PT   reduced bone density.
XX
PS   Disclosure; Page 498-501; 603pp; English.
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XX
CC   The invention relates to novel transgenic animals expressing the high
CC   bone mass (HBM) gene, expressing the corresponding wild type HBM gene,
CC   comprising an alteration of the gene encoding LRP5 or LRP6, or expressing
CC   an LRP5 that is modulated by an altered gene control sequence introduced
CC   by homologous or non-homologous recombination. The transgenic animals are
CC   for the study of bone density modulation or bone mass modulation. The
CC   invention has osteopathic and cytostatic activity. The polynucleotides of
CC   the invention may have a use in gene therapy. The transgenic animals and
CC   nucleic acids are for the study of bone density modulation, where the
CC   bone mass is modulated relative to non-transgenic animals of the same
CC   species in more than one parameter selected from bone density, bone
CC   strength, trabecular number, bone size, or bone tissue connectivity. The
CC   transgenic animals, nucleic acids and methods are useful for identifying
CC   molecules involved in bone development, and for developing pharmaceutical
CC   compositions, which may be employed for treating or preventing bone
CC   diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or
CC   neoplasms of the bone. The transgenic animals and nucleic acids are also
CC   useful in methods for diagnosing diseases involved in bone development,
CC   or characterised by reduced bone density or mass. The present sequence is
CC   used in the exemplification of the invention
XX
SQ   Sequence 7680 BP; 2081 A; 1981 C; 1862 G; 1756 T; 0 U; 0 Other;

  Query Match             95.2%;  Score 7423;  DB 7;  Length 7680;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7432;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy        349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy        409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy        469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
              |||||||||||| ||| |||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy        529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

Qy        589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

Qy        649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy        709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy        769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480

Qy        829 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 540

Qy        889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy        949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

Qy       1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
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Db      661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy     1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy     1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy     1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG 1248
            |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db      841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGTTGAAGACACAAGG 900

Qy     1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy     1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
            ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy     1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
            ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db     1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy     1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy     1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy     1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy     1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy     1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy     1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy     1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
            |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db     1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy     1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy     1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy     1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy     2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy     2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy     2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy     2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy     2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy     2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy     2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy     2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

Qy     2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

Qy     2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy     2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

Qy     2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy     2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy     2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

Qy     2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

Qy     2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

Qy     2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

Qy     3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy     3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy     3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880
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Qy       3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy       3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy       3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy       3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy       3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy       3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db       3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy       3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy       3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy       3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy       3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy       3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy       3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600

Qy       3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
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Db       3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy       4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy       4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy       4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy       4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy       4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy       4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy       4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy       4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy       4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy       4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy       4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4320

Qy       4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy       4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy       4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy       4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy       4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

Qy       4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

Qy       5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy       5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800

Qy       5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy       5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy       5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
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Db       4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

Qy       5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy       5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
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Db          5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy          5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy          5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
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Db          5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy          5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy          5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy          5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400

Qy          5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
                 ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db          5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy          5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5461 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5520

Qy          5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
                 |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db          5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

Qy          5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
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Db          5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

Qy          5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
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Db          5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy          6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy          6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
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Db          5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

Qy          6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

Qy          6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy          6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy          6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy          6409 GCAACAAATGATCTTTGAGGAACATGGTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6061 GCAACAAATGATCTTTGAGGAACATGGTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy          6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

Qy          6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6181 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

Qy          6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300

Qy          6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360

Qy          6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

Qy          6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
                 |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db          6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

Qy          6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

Qy          6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

Qy          6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

Qy          7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6661 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 6720

Qy          7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

Qy          7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6781 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840

Qy          7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6841 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 6900

Qy          7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960

Qy          7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

Qy          7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080

Qy          7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

Qy          7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

Qy          7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260
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Qy       7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

Qy       7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy       7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440

Qy       7789 CAGTACT 7795
              |||||||
Db       7441 CAGTACT 7447

RESULT 14
ACF12859
ID   ACF12859 standard; cDNA; 7680 BP.
XX
AC   ACF12859;
XX
DT   10-SEP-2003  (first entry)
XX
DE   Human cervical cancer cell marker encoding cDNA SEQ ID NO:63.
XX
KW   Human; cervical cancer; cervical cancer marker; cancer therapy;
KW   detection; gene therapy; vaccine; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2002101075-A2.
XX
PD   19-DEC-2002.
XX
PF   12-JUN-2002; 2002WO-US018638.
XX
PR   13-JUN-2001; 2001US-0298155P.
PR   13-JUN-2001; 2001US-0298159P.
PR   14-NOV-2001; 2001US-0335936P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Schlegel R,  Chen Y,  Zhao X,  Monahan JE,  Kamatkar S;
PI   Gannavarapu M,  Glatt K,  Hoersch S;
XX
DR   WPI; 2003-156967/15.
DR   P-PSDB; ABR92078.
XX
PT   New isolated nucleic acid molecule useful for detecting, characterizing,
PT   preventing and treating human cervical cancers, in various prognostic and
PT   diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
XX
PS   Claim 4; Page 209-212; 386pp; English.
XX
CC   ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I)
CC   given in ABR92047 to ABR92164. A higher level of expression of (I) than
CC   normal indicates the presence of cervical cancer. Also described: (1) a
CC   vector (II) containing (I); (2) a host cell (III) containing (I); and (3)
CC   assessing (M1) whether a patient is afflicted with cervical cancer,
CC   comprising comparing the level of expression of a marker in a patient's
CC   sample, and the normal level of expression of the marker in a control non
CC   -cervical cancer sample, where a significant increase in the level of
CC   expression of the marker in the patient's sample relative to that in the
CC   control sample is an indication that the patient is afflicted with
CC   cervical cancer. (I) has cytostatic activity, and can be used in gene
CC   therapy and in vaccines. (I) is useful in detecting, characterising,
CC   preventing and treating human cervical cancers. (I) may also be used in
CC   various prognostic and diagnostic assays, pharmacogenomics and in
CC   monitoring clinical trials
XX
SQ   Sequence 7680 BP; 2081 A; 1981 C; 1862 G; 1756 T; 0 U; 0 Other;

  Query Match             95.2%;  Score 7423;  DB 7;  Length 7680;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7432;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy        349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy        409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy        469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
              |||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy        529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

Qy        589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

Qy        649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy        709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy        769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480

Qy        829 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 540

Qy        889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy        949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

Qy       1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy       1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy       1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy       1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGATGCAGTGGCTGAAGACACAAGG 1248
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGATGCAGTGGTTGAAGACACAAGG 900

Qy       1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy       1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020
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Qy   1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy   1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy   1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy   1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy   1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy   1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380

Qy   1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1440

Qy   1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy   1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy   1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy   1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy   2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy   2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy   2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy   2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy   2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy   2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy   2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy   2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

Qy   2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

Qy   2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy   2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

Qy   2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy   2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy   2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

Qy   2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

Qy   2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

Qy   2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

Qy   3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy   3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy   3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy   3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy   3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy   3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy   3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   3061 TGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy   3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy   3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
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                   |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db            3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy            3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy            3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy            3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy            3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
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Db            3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy            3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy            3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            3541 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600

Qy            3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy            4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy            4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy            4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy            4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy            4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy            4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy            4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy            4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy            4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy            4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy            4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            4261 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4320

Qy            4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy            4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy            4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy            4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy            4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

Qy            4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680

Qy            5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy            5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            4741 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 4800

Qy            5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy            5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            4861 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 4920

Qy            5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            4921 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 4980

Qy            5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5040

Qy            5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy            5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy            5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy            5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5280

Qy            5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db            5281 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT 5340

Qy            5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            5341 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5400
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Qy          5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
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Db          5401 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA 5460

Qy          5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
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Db          5461 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5520

Qy          5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
                 |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db          5521 CTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5580

Qy          5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5640

Qy          5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5641 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 5700

Qy          6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5701 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5760

Qy          6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5761 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 5820

Qy          6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 5880

Qy          6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 5940

Qy          6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy          6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6001 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6060

Qy          6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy          6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6121 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6180

Qy          6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6588
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6181 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 6240

Qy          6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6648
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300

Qy          6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6301 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6360

Qy          6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6361 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6420

Qy          6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
                 |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db          6421 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGG 6480

Qy          6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

Qy          6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

Qy          6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

Qy          7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy          7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6721 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 6780

Qy          7129 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7188
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6781 CTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840

Qy          7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6841 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 6900

Qy          7249 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960

Qy          7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020

Qy          7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080

Qy          7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7081 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140

Qy          7489 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

Qy          7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260

Qy          7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7261 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7320

Qy          7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380

Qy          7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440

Qy          7789 CAGTACT 7795
                 |||||||
Db          7441 CAGTACT 7447


RESULT 15
ACA64817
ID   ACA64817 standard; DNA; 7680 BP.
XX
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AC   ACA64817;
XX
DT   27-JUN-2003  (first entry)
XX
DE   Human fibronectin DNA corresponding to X02761.
XX
KW   Human; chronic inflammatory joint disease; infection; tumour;
KW   antiinflammatory; cytostatic; antiarthritic; antirheumatic;
KW   immunosuppressive; gene therapy; etiological pathogenicity; ds.
XX
OS   Homo sapiens.
XX
PN   DE10127572-A1.
XX
PD   05-DEC-2002.
XX
PF   30-MAY-2001; 2001DE-01027572.
XX
PR   30-MAY-2001; 2001DE-01027572.
XX
PA   (PATH-) PATHOARRAY GMBH.
XX
PI   Haeupl T,  Ungethuem U,  Blaess S;
XX
DR   WPI; 2003-240797/24.
XX
PT   Reagents for diagnosis, study and therapy of chronic inflammatory joint
PT   and other diseases, comprises any of many specified genes or derived
PT   proteins.
XX
PS   Claim 1; Page; 12pp; German.
XX
CC   This invention describes a novel reagent for diagnosis, molecular
CC   definition and therapy of chronic inflammatory joint diseases, and other
CC   inflammatory disorders, infective or tumour diseases in humans. The
CC   products of the invention have antiinflammatory, cytostatic,
CC   antiarthritic, antirheumatic and immunosuppressive activity and can be
CC   used for gene therapy. The reagent of the invention and any proteins and
CC   antibodies derived from it, are used (i) for analysing tissue and blood
CC   samples for medical diagnosis; (ii) for diagnosis and characterisation of
CC   chronic joint diseases, on the basis of molecular characterisation, and
CC   determining the etiological pathogenicity principle of as yet
CC   uncharacterised inflammatory diseases, also monitoring progression and/or
CC   treatment of disease, and optimisation of therapy and (iii) for
CC   developing treatments for inflammatory diseases, particularly of joints,
CC   infections and tumours. ACA64801-ACA64965 represent human polynucleotides
CC   used in the method of the invention
XX
SQ   Sequence 7680 BP; 2081 A; 1981 C; 1862 G; 1756 T; 0 U; 0 Other;

  Query Match             95.2%;  Score 7423;  DB 7;  Length 7680;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 7432;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy        349 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA 60

Qy        409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120

Qy        469 GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 528
              |||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180

Qy        529 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240

Qy        589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300

Qy        649 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360

Qy        709 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420

Qy        769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTT 480

Qy        829 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 540

Qy        889 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 600

Qy        949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

Qy       1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 720

Qy       1069 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCAC 780

Qy       1129 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 1188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA 840

Qy       1189 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG 1248
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db        841 CTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGTTGAAGACACAAGG 900

Qy       1249 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 960

Qy       1309 AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        961 AACCCAGACTTACGGTGGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1020

Qy       1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1428
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1021 TGGCAGGACGTTCTACTCCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAG 1080

Qy       1429 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140

Qy       1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1548
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTTCAGACTCAAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 1200

Qy       1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1260

Qy       1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320

Qy       1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1380
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Qy       1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGAATGGAC 1788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGAATGGAC 1440

Qy       1789 ATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1848
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db       1441 ATGCATTGCCTACTCGCAACTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT 1500

Qy       1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1560

Qy       1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1620

Qy       1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 1680

Qy       2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 1740

Qy       2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 1800

Qy       2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 1860

Qy       2209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 1920

Qy       2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 1980

Qy       2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACACCTGTGAC 2040

Qy       2389 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2100

Qy       2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2160

Qy       2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGA 2220

Qy       2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280

Qy       2629 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340

Qy       2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400

Qy       2749 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460

Qy       2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2520

Qy       2869 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2928
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCA 2580

Qy       2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640

Qy       2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700

Qy       3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 2760

Qy       3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 3168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820

Qy       3169 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 3228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 GTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGAGAGCAA 2880

Qy       3229 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940

Qy       3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000

Qy       3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060

Qy       3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120

Qy       3469 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180

Qy       3529 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG 3588
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db       3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240

Qy       3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC 3300

Qy       3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360

Qy       3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420

Qy       3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3480

Qy       3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAG 3540

Qy       3889 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3541 AATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600

Qy     3949 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 3660

Qy     4009 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3661 TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 3720

Qy     4069 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3721 TCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 3780

Qy     4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3781 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840

Qy     4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3841 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 3900

Qy     4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 3960

Qy     4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4368
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3961 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTC 4020

Qy     4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080

Qy     4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140

Qy     4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4548
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4141 CCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200

Qy     4549 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4608
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4201 CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGT 4260

Qy     4609 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4261 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4320

Qy     4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4321 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4380

Qy     4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4788
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4381 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG 4440

Qy     4789 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4848
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4441 CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4500

Qy     4849 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4501 CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4560

Qy     4909 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4561 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4620

Qy     4969 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 5028
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4621 CCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC 4680
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Qy     5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088
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Db     4681 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 4740

Qy     5089 GTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC 5148
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208
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Db     4801 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 4860

Qy     5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328
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Qy     5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA 5388
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Qy     5389 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448
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Db     5041 TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5100

Qy     5449 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5508
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5101 CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGT 5160

Qy     5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568
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Db     5161 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5220

Qy     5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
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Qy     5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688
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Qy     5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 5748
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Qy     5749 GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808
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Qy     5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868
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Qy     5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928
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Qy     5929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988
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Qy     5989 CAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048
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Qy     6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 6108
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Qy       6109 GGTCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168
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Qy       6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGAGCCCCTGATTGG 6228
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Qy       6229 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288
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Qy       6289 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6348
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Db       5941 ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG 6000

Qy       6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 6408
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Qy       6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 6120

Qy       6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCA 6528
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Qy       6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
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Qy       6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
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Db       6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540

Qy       6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6948
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Db       6541 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 6600

Qy       6949 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 7008
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Db       6601 CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATG 6660

Qy       7009 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
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Qy       7069 TGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC 7128
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Qy       7189 TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
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Qy       7369 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7428
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Qy       7429 TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7488
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Db       7141 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7200

Qy       7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
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Qy       7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
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Qy       7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
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Qy       7789 CAGTACT 7795
              |||||||
Db       7441 CAGTACT 7447

Search completed: March  7, 2004, 08:59:22
Job time : 2569 secs
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